Perfect score:

Sequence:

OM nucleic

Run on:

Scoring table:

Searched:

Database

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WHE0364_A03_A06ZS Wheat cold-stressed seedling cDNA library
Triticum aestivum cDNA clone WHE0364_A03_A06, mRNA sequence.
BE490056
EB490056.1 GI:9609589
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Anderson, O.D., Chao, S., Chol, D.W., Close, T.J., Fenton, R.D., Han P.S., Hsia, C.C., Kang, Y., Lazo, G.R., Miller, R., Rausch, C.J., Seaton, C.L. and Tong, J.C.
The structure and function of the expressed portion of the wheat genomes - Cold-stressed seedling cDNA library Unpublished (2000)
Unpublished (2000)
US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center
BOOD Buchanan Street, Albany, CA 94710, USA
BEO40022 OC10E10 O
AI293432 LP06566.5
BF479168 L48-2827
AQ330709 nbxb0047D
BG912909 602807305
AIZ59731 LP03218.5
AL380410 MEBB52C08
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AS985567 200267P21
AU102211 AU102211
BI546997 603190218
AI665559 605012402
BI075779 IPL_2L_BO
BF189425 235000 MA
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                                                                                                             R15016 yf86a07.r1
AL099337 Drosophil
B1995281 1031026A1
AV401151 AV401151
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BE584493 7-10D-20
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AA997882 UI-R-C0-h
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/cultivar="Chinese Spring"
/db_xref="taxon:4565"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: oandersn@pw.usda.gov
Sequence have been trifinmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: Stratagene SK primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALIGNMENTS
                                                AQ330709
BG912909
                                                                                                               R15016
CNS010RJ
BF444536
AV401151
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AU161359
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BG594730 EST493200
AW651434 EST329888
BE432955 EST406033
BB432832 EST399463
BE432502 EST3999631
BF254425 HVSMEF000
BF354425 HVSMEF000
BF33734 BGGCC23TR
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2307.302 Million cell updates/sec
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                                                                                                               October 10, 2002, 02:11:42; Search time 1596.96 Seconds
                                                                                                                                                                                              273
1 cttcctcntgcacgcttcgn......tcctggttggccaangcgtt 273
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                  GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                           13736207 seqs, 6748477542 residues
                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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em_gss_inv:*
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Best Local 9
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/note="Vector: Lambda Uni-ZAP XR, excised phagemid; Site_1: EcoRI; Site_2: XhoI; Seeds were surface-sterilized, germinated and grown aseptically in the dark at room temperature on filter paper with water, nystatin and cefotaxime in covered crystallization dishes. Five-day old seedlings were transferred to 5 cold room and kept for 48 hr. The tissue, total RNA, and poly(A) RNA were prepared, a cDNA library was made, and the cDNA clones were in vivo excised to give pBluescript phagemids in the TJ Close lab (Choi, Close, Fenton) at the University of California, Riverside. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     684 bp mRNA linear EST 12-APR-2001 EST493599 cSTS Solanum tuberosum cDNA clone cSTS8J4 5' sequence, BG594921
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1 (bases 1 to 684)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            van der Hoeven, R., Bezzerides, J., Sun, H., Cho, J., Chiemingo, A., Bougri, O., Buell, C.R., Ronning, C., Tanksley, S. and Baker, B. Generations of ESTs from sprouting potato eyes Unpublished (2000)

Contact: Cathy Ronning
The Institute for Genomic Research
For clone info: please contact Research Genetics, Libraries
Division tel 1.800-711-6195, email cdna@resgen.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90 gtcgtcaaacagaccggccagaagcctcactacgtcggacactccatggggacgctggtg 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                             30 tactggaactggtcctgggatgacctggtagtcaacgacctgccggccatggtcgacttc 89
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0
                                                                                                                                                                                                                                                                                                                                   Score 147.4; DB 10; Length 618; Pred. No. 1.7e-21;
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/clone_lib="cSTS"
/tisoue_type="sprouting eyes from tube
/dev_stage="12-14 weeks post harvest"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                           44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Solanum tuberosum"
/cultivar="Kennebec"
/db_xref="taxon:4113"
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                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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79.68;
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Best Local Similarity 79.69
Matches 172; Conservative
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Solanum tuberosum
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Solanum tuberosum
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
E 1 (bases 1 to 746)
S van der Hoeven, R., Bezzerides, J., Sun, H., Cho, J., Chiemingo, A.,
Bougri, O., Buell, C.R., Ronning, C., Tanksley, S. and Baker, B.
Generations of ESTs from sprouting potato eyes
Uppublished (2000)
Contect: Cathy Ronning
The Institute for Genomic Research
For clone info: please contact Research Genetics, Libraries
Division tel 1-800-711-6195, email cdna@resgen.com
Seq primer: Mi3F-R.
taken from tubers. The tubers were incubated at 26C in the dark for 2-3 weeks prior to sprouting. The eyes were frozen in liquid nitrogen immediately upon removal from tubers."
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/dev_stage="12-14 weeks post harvest"
/dev_stage="12-14 weeks post harvest"
/dab_host="SOLR"
/note="Weetor: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI; Various sizes of sprouting eyes (2mm to 15mm) were
taken from tubers. The tubers were incubated at 2cc in the
dark for 2-3 weeks prior to sprouting. The eyes were
frozen in liquid nitrogen immediately upon removal from
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                                                                                                                                                                                                                                                                                                                                                         88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                89 cgtcgtcaaacagaccggccagaagcctcactacgtcggacactccatggggacgctggt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29 ctactggaactggtcctgggatgacctggtagtcaacgacctgccggccatggtcgactt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       268 TGTCTTTAAACAAACTGGGCAGAAAATTCACTATATAGGCCATTCAATGGGAACCTTGAT
                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                 Length 684;
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                                                                                                                                                                                                                                           Score 96.8; DB 10;
Pred. No. 6.7e-11;
0; Mismatches 86;
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/cultivar="Kennebec"
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/clone="cSTS8E14"
/clone_lib="cSTS"
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ilarity 62.9%;
Conservative
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/creativar="Lycopersicon esculentum"
/cultivar="TA496"
/du_rref="Laxon:4081"
/dlone="clEf1661"
/clone="clEf1661"
/clone="clEf1661"
/clone="clEf1661"
/clone="taxon:4081"
/clone="taxon:408
                                                                                                                                                                                                                                                                                                                                                                    AW651434 Lomato germinating seedlings, TAMU Lycopersicon esculentum cDNA clone cLE116L17 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 643)
Alcala,J., Vrebalov,J., White,R., van der Hoeven,R.S, Holt,I.E.,
Liang,F., Hansen,T.S., Craven,M.B., Bowman,C.L.; Ronnning,C.M.,
Nierman,W., Fraser,C.M., Glovannoni,J.J., Martin,G.B. and Tanksley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lycopersicon esculentum
Sukaryota, Vitidiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
     133 TGTCTTTAAACAAACTGGGCAGAAAATTCACTATATATGCCATTCAATGGGAACCTTGAT 192
                                                          149 ggcgctggcggccttctcggaggccgggtgagccagctgaaatccgcgggcgctgct
                                                                                                                 193 AGCGTTGGCGTCCTTTTCAGAAGGGAAACAAATAGACAAGGTAAAATCAGCAGCCTTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
                                                                                                                                                                                                      cacgccggtggcctacctcgnccacatnaacancccaatnggaatcctggt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Generation of ESTs from germinating tomato seed Unpublished (2000)
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illarity 61.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BG098681 375 bp mRNA linear EST 29-JAN-2001 EST463200 sprouting eyes/shoots Solanum tuberosum cDNA clone cSTC5E1 5' sequence, mRNA sequence.
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and Baker
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota; Viridiplantae; Streptophyta; Core eudicots;

Aspermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Asteridae; euasterids I; Solanales; Solanaceae; Solanum.

1 (bases 1 to 375)

van der Hoeven, R.S., Bezzerides, J., Cho, J., Utterback, T., Hansen, C.L., Bougri, O., Buell, C.R., Ronning, C.M., Tanksley, S.D. and Bake)
                                                                                                                                                                                                89 cgtcgtcaaaacagaccagaccagaagcctcactacgtcggacactccatggggacgctggt 148
                                                                                                                                                                                                                                   133 TGTCTTTAAACAAACTGGGCAGAAAATTCACTATATAGGCCATTCAATGGGAACCTTGAT 192
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                                                                                                                                                                                                                                                                                                                                                                       193 AGCGTTGGCGTCCTTTTCAGAAGGGAAACAAATAGACAAGGTAAAATCAGCAGCCTTGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Generation of ESTs from potato sprouting eyes/shoots
Unpublished (2001)
Contact: Cathy Ronning
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              For clone info: please contact Research Genetics, I
Division tel 1-800-711-6195, email cdna@resgen.com
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                   Indels
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/cultivar="Rennebec"
/cultivar="Rennebec"
/clone="csTG5E"
/clone_lib="sprouting eyes/shoots"
/fissue_type="sprouting tubers"
/dev_stage="12-14 weeks post harvest"
/lab_host="SolR"
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62.5%; Pred. No. 1.3e-10;
No. 6.8e-11;
smatches 86;
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Matches 145; Conservative
                                146; Conservative
Best Local Similarity
Matches 146; Conserv
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BE432838.1 GI:9430777
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64.6%;
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                                                                                                       BE434955 564 bp mRNA linear EST 18-MAY-2001 EST406033 tomato breaker fruit, TIGR Lycopersicon esculentum cDNA
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                                                                                                                                                                                                                       Lycopersicon esculentum
Bukaryota, Vizidiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots;
Asteridae, euasterids I; Solanales, Solanaceae, Solanum;
                                                                                                                                                                                                                                                                                                         1 (bases 1 to 564)
Jaclada, J. Vrebalov, J., White, R., van der Hoeven, R.S., Holt, I.E.,
Liang, F., Hansen, T.S., Craven, M.B., Bowman, C.L., Ronning, C.M.,
Nierman, W., Fraser, C.M., Martin, G.B., Giovannoni, J.J. and Tanksley
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                                                                                                                                                                                                                                                                                                                                                                             ,S.D. Generation of ESTs from tomato fruit tissue, breaker stage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
5 prime sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 564;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="tomato breaker fruit, TIGR"
/tissue_lip="tomato breaker"
/dev_stage="breaker"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. .564
/organism="Lycopersicon esculentum"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="cLEG24M2"
602 AGTCCAATTGCTTATTTGAGCCATATGACCACTGCACTTGG 642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 82; DB 10;
Pred. No. 8.2e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Clemson University Genomics Institute
Clemson University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                       clone cLEG24M2, mRNA sequence.
BE434955
BE434955.1 GI:9432798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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Best Local Similarity 63.9%;
Matches 124; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | || | | | || || AGTCCAATIGCTIA 559
                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: CUGI
                                                                                                                                                                                                                                                                                            Lycopersicon.
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                                                                                                                                                                                                           tomato.
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ORGANISM
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ORIGIN
                                                                                                                     DEFINITION
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JOURNAL
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                                                                                                                                                       ACCESSION
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BE432838
                                                                                   BE434955
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EST 18-MAY-2001
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                                                                                                                                                                                                                                                                                                                                      1 (bases I to 544)
Alcala,J., Vrebalov,J., White,R., van der Hoeven,R.S., Holt,I.E.,
Liang,F., Hansen,T.S., Craven,M.B., Bowman,C.L., Ronning,C.M.,
Nierman,W., Fraser,C.M., Martin,G.B., Giovannoni,J.J. and Tanksley
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                             TIGR Lycopersicon esculentum cDNA
                                                                                                                                                                                                                               Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90 gtcgtcaaacagaccggccagaagcctcactacgtcggacactccatggggacgctggtg 149
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                                                                                                                                                                                                                      Lukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheo, Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30 tactggaactggtcctggatgacctggtagtcaacgacctgccggccatggtcgacttc
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clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:4081"
/clone="clEG11C5"
/clone_lib="tomato breaker fruit, TIGR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Lycopersicon esculentum"
/cultivar="TA496"
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Pred. No. 8.3e-07;
0; Mismatches 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="Pericarp"
/dev_stage="breaker"
/lab_host="SOLR"
BE432838 544 bp EST399463 tomato breaker fruit,
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                                               clone cLEG11C5, mRNA sequence.
BE432838
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                                                                                                                                                                                                     Lycopersicon esculentum
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/note="Vector: pBluescriptSKmCUadapt; Site_1: EcoR1; Site_2: XhoI; Fruit were harvested at the breaker stage (first sign of lycopene accumulation on the blossom end of the fruit). Fruit were cut in half and the seeds and locules were discarded prior to freezing the pericarp." 98 c 142 g 173 t 1 others
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; Triticeae; Hordeum.
; (Losse, 1.038)
Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Begum, D., Frisch, D., Yu, Henry, D., Palmer, M., Rambo, T., Simmons, J., Choi, D.W., Fenton, R.D., Oates, R. and Main, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HVSMEf0003P17f Hordeum vulgare seedling root EST 22-OCT-2001 (Etiolated and unstressed) Hordeum vulgare cDNA clone HVSMEf0003P17f, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
                                             l (bases 1 to 577)
Alcala,J., Vrebalov,J., White,R., van der Hoeven,R.S., Holt,I.E., Liang,F., Hansen,T.S., Craven,M.B., Bowman,C.L., Ronning,C.M., Nierman,W., Fraser,C.M., Martin,G.B., Giovannoni,J.J. and Tanksley
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          146 ggtggcgctggcggccttctcggagggccgggtggtgagccagctgaaatccgcgggcgct 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         352 ATCNTTCCAAAACAAACTGGACAGAAATACACTATGTTGGTCATTCAATGGGAACTTT 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        292 TACTGGAATTGGTCATGGGATGAATTGATTGTTCATGATTTACCATCTGTTATTGACTTT 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30 tactggaactggtcctgggatgacctggtagtcaacgacctgccggccatggtcgacttc 89
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                                                                                                                                                                                                                                                                                           100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="tomato breaker fruit, TIGR"
                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Lycopersicon esculentum"/cultivar="TA496"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 72.8; DB 10;
Pred. No. 7e-06;
0; Mismatches 92;
                                                                                                                                                                                                                                             Clemson University Genomics Institute
Clemson University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="Pericarp"
/dev_stage="breaker"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:4081"
/clone="cLEG8D15"
                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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BF254425.3 GI:16315084
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59.1%;
                                                                                                                                                                                               (2000)
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Matches 139; Conservative
                                                                                                                                                                                                                                                                                                                                              prime sequence.
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                                                                                                                                                                                             Unpublished (;
Contact: CUGI
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ORIGIN
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JOURNAL
COMMENT
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/note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xhol:
SeedS were surface sterilized then germinated under axenic
Conditions in the dark at room temperature on filter paper
with water, nystain and cefotaxime in covered
crystallization dishes. Five-day old seedling roots were
then harvested, total RNA was prepared, poly(A) RNA was
purified, one primary unamplified cDNA library was made,
and 1 million pfu were in vivo excised to give pBluescript
SK(-) CDNA phagemids. These steps were performed in the TJ
Close laboratory at the University of California,
Riverside (Choi, Close, Fenton). Phagemids were plated and
picked at the clemson University Genomics Institute (CUGI)
(Begum, Palmer, Firsch, Arkins and Wing). Plasmid DNA
preparations, DNA sequencing and sequence analysis were
performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates
vector, sequence and contains a minimum of 100 bases of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ä
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Development of a genetically and physically anchored EST resource for barley genomics: Morex unstressed seedling root cDNA library Unpublished (2001)
On Nov 16, 2000 this sequence version replaced g1:13117126.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="Hordeum vulgare seedling root EST library HVcDNA0007 (Etiolated and unstressed)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 caacgacctgccggccatggtcgacttcgtcgtcaaacagacc---ggccagaagcctca 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            395 TACCTCGCTCACTCCAGATGATCCGGAGTACTGGAACTGGACGTGGGACCAACTTGCTGC 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           phred value 20 or above. For more details on library preparation and sequence analysis see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      179 ggtgagccagctgaaatccgcggcgctgctcacgccggtggcctacctcgnccacatnaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             455 CTATGATCTTCCTGCCGTGCTTCAGTTTGTCTATGATCACAGGAGGCCAGAAAGTCCA
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Pred. No. 0.00035;
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                                                                                                                                                                                                        Člemson, SC 29634, USA
                                                                                                                                              Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="Seedling root"
/lab_host="TJC121"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Hordeum vulgare"
/cultivar="Morex"
                                                                                                                                                                                                                                                                                                                                                      Seq primer: AATTAACCCTCACTAAAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:4513"
/clone="HVSMEf0003P17f"
                                                                                                                                                                                                                                                                                                                                                                                    High quality sequence stop: 664
Location/Qualifiers
                                                                                                                                                                                                                                                                                         Email: rwing@clemson.edu
Total hq bases = 561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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56.7%;
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                                                                                                                                                                                                                                      Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                      Contact: Wing RA
                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. 830
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BH537343.1 GI:17773756
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es 90; Conserv
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KEYWORDS
SOURCE
ORGANISM
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ORIGIN
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Matches
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COMMENT
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                                                                                                                                             AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="tomato breaker fruit, TIGR"
/clone_lib="tomato breaker fruit, TIGR"
/tissue_type="Pericarp"
/dev_stage="pericarp"
/dev_stage="berlearp"
/lab_host="SOLR"
/lab_host="
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                    EST 18-MAY-2001
                                                                                                                                                                                                                                                                                        Lycopersicon esculentum
Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots;
Asteridae, euasterids I; Solanales, Solanaceae; Solanum;
                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 398)
Abdala,J., Vrebblov,J., White,R., van der Hoeven,R.S., Holt,I.E.,
Liang,F., Hansen,T.S., Craven,M.B., Bowman,C.L., Ronning,C.M.,
Nierman,W., Fraser,C.M., Martin,G.B., Glovannon1,J.J. and Tanksley
                                                      398 bp mRNA linear EST 18-MAY-200 EST407344 tomato breaker fruit, TIGR Lycopersicon esculentum cDNA clone cLEG31C20, mRNA sequence.
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Generation of ESTs from tomato fruit tissue, breaker stage
Unpulished (2000)
Contact: CUGI
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Pred. No. 0.0021;
0; Mismatches 42; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .398
/organism="Lycopersicon esculentum"
/cultivar="TA496"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:4081"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     prime sequence.
Location/Qualifiers
                                                                                                                                                                      BE436266
BE436266.1 GI:9434109
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T46320.1 GI:2763011
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Best Local Similarity 67.2
Matches 86; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                           Lycopersicon.
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                                                                                                                                                                                                                                                             tomato.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     source
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ORIGIN
                                                                                                            DEFINITION
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T46320
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JOURNAL
COMMENT
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AUTHORS
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KEYWORDS
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KEYWORDS
GOURCE
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denes galore: a summary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis CDNA clones plant Physiol. 106, 1241-1255 (1994)

Enarge-scale partial sequencing of anonymous Arabidopsis CDNA clones plant Physiol. 106, 1241-1255 (1994)

Enarge-scale partial sequencing of anonymous Arabidopsis CDNA clones plant Physiol. 106, 1241-1255 (1994)

On Jan 9, 1998 this sequence version replaced gi:934542.

Contact: Thomas Newman

Michigan State University

Michigan State University

Michigan State University, Plant Biology Bldg., E.

Lansing, Mi
Tel: 517-353-0854

Fax: 517-353-0868

Email: 22313tcneibm.cl.msu.edu
Seq primer: T7 dye primer.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /un-rel_table_lambda-PRL2"
/clone=1141F5T7"
/clone=11b="Lambda-PRL2"
/clone=11b="Lambda-PRL2"
/note="Vector: lambda zip-Lox; Site_1: Sal; Site_2: Not; Lambda PRL2 is a cDNA library derived from equal quantities of 4 pools of mRNA. The mRNA sources were 1) 7 day germinated etiolated seedlings; 2) tissue culture grown roots; 3) staged plants half with 24 hour light grown roots; 3) staged plants half with 24 hour light cycle, half on 16 hr light, 8 hour dark-rosettes; 4) same plants as 3 but aerial tissue (stems, flowers and sliques. The vector is BRL's lambda Zip-Lox. The cDNA inserts were directionally cloned with Sal-Not arms using oligo dT primed cDNA. 83 t 8 others
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis. 1 (bases I to 213) Newman, T., deBruijn, F. J., Green, P., Keegstra, K., Kende, H., McIntosh, L., Ohlrogge, J., Raikhel, N., Somerville, S., Thomashow, M., Retzel, E. and Somerville, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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Brusryota, Viridiplantae; Streptophyta; Embryophyta: Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
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llarity 58.8%; Pred. No. 0.0051;
Conservative 0; Mismatches 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Arabidopsis thaliana"
/strain="var columbia"
/db_xref="taxon:3702"
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PICI_24_G11.bl_A002 Pathogen-infected compatible 1 (PIC1) Sorghum bicolor cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequences have been trimmed to exclude PolyA, vector, and regions below Phred quality 16. The threshold for highest quality sequence is 20. Three-prime sequences, which are obtained with PolyTMix or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukāryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoldeae; Andropogoneae; Sorghum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 623)
Cordonier-Pratt, M., Gingle, A., Fang, G.C., Dean, R., Wing, R.,
Sudman, M. and Pratt, L.H.
An EST database from Sorghum: plants infected with a compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The University of Georgia
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
TTE: 706 542 1860
Fax: 706 542 1805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 53.8; DB 12; Length 680;
Pred. No. 0.068;
0; Mismatches 42; Indels 0
                /clone_lib="CUGI Rice BAC Library"
/tissue_type="Leaf"
/lab_host="E. coli DH10B"
 /clone-"nbxb0081N07f"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (2002)
Contact: Cordonnier-Pratt MM
Department of Botany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BM324154
BM324154.1 GI:18062592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: mmpratt@uga.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19.7%;
65.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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BM324154
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nbxb0081N07f CUGI Rice BAC Library Oryza sativa genomic clone
nbxb0081N07f, DNA sequence.
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I (bases I to 680)

Wing, R.A. and Dean, R.A.

A BAC End Sequencing Framework to Sequence the Rice Genome Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                 /Glone_lbw=BoGC"
/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
genomic DNA inserted into pHOS1 using BstXI linkers"
it / 154 q 232 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25 agetetactggaactggteetgggatgaectggtagteaacgaectgeeggeeatggteg 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85 acttcgtcgtcaaacagaccggccagaagcctcactacgtcggacactccatgggg 140
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 737;
            Town, C.D., Van Aken, S., Utterback, T. and Fraser, C.M. Whole genome shotgun sequencing of Brassica oleracea Unpublished (2001) Other, GSS: BOGCC23TF Contact: Chris Town
                                                                                                                                                                 Email: cdtownetigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.
                                                                                                                   9712 Medical Center Drive, Rockville, MD 20850, USA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 55.2; DB 12; Length Pred. No. 0.035; 0; Mismatches 38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                  Location/Qualifiers
1. 737
/organism="Brassica oleracea"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Wing RA
Clemson University Genomics Institute
Clemson University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Oryza sativa"
/strain="Japonica"
/cultivar="Nipponbare"
/db_xref="taxon:4530"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: rwing@clemson.edu
Seg primer: TAATACGACTCACTATAGGG
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     High quality sequence stop: 368.
Location/Qualifiers
                                                                                                                                                                                                                                                                                        /strain="TO1000DH3"
/db_xref="taxon:3712"
/clone="BOGCC23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AQ690237.1 GI:5331405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 20.2%;
Best Local Similarity 67.2%;
Matches 78; Conservative (
(bases 1 to 737)
                                                                                                                                   Tel: 301-838-3523
Fax: 301-838-0208
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KEYWORDS
SOURCE
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AQ690237/c
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COMMENT
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            AUTHORS
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Search completed: October 10, 2002, 02:41:26 Job time: 1784 sec
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                                                                                                                                                    /crganism="Sorghum bicolor"
/cultivar="BTx623"
/dultivar="BTx623"
/dultivar="BTx623"
/dultivar="BTx623"
/clone_lip="Pathogen-infected compatible 1 (PIC1)"
/tissue_type="Leaves"
/dev_stage="4-week-old seedlings infected with
Colletorichum graminicola" ISK(-) from Lambda Zap II;
/note="Vector: pBluescript II SK(-) from Lambda Zap II;
/note="Vector: pBluescript II SK(-) from Lambda Zap II;
Site_1: XhoI; Site_2: EcoRI; Four-week-old sorghum
seedlings were sprayed with spore suspension prepared from
3-week-old FRMA2I, a sorghum isolate of the anthracnose
pathogen Colletotrichum graminicola. Inoculated plants
were kept in a 25 C dark growth chamber with 100% relative
humidity for 24 hr, followed by 12/12 hr of light/dark
cycle at 25 C with 90% relative humidity for another 24
hr. All leaves were harvested and quick frozen with liquid
nitrogen and stored in a -80 C freezer. The library was
made from poly-A RNA in the cloning vector lambda ZaP II.
Clones to be sequenced were prepared by mass excision.
WARNING: While most or all ESTs are expected to derive
from the host plant, no effort was made to eliminate ESTs
deriving from the pathogen.
58 a 116 c 139 g 210 t
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1 (bases 1 to 557)

2 van der Hoeven, R., Bezzeridaes, J., Sun, H., Cho, J., Chiemingo, A., Bougri, O., Buell, C.R., Ronning, C., Tanksley, S. and Baker, B. Generations of ESTs from sprouting potato eyes

Contact: Cathy Ronning

The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63 aacgacctgccggccatggtcgacttcgtcgtcaaacagaccggccagaagcctcactac 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                180 TCTACTCTCTCTGTTCATGATAAGCTTTTCTGGGAATGGAGTTGGCAAGACCTTGCTGAA 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              240 TACGATGTTTTGGCAATGTTAAGCTATGTATATACAATTACACTCCAAAATTTCATAT 299
T7 sequencing primer, are presented as the reverse complement.
Seq primer: JEN REV
High quality sequence stop: 573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 19.6%; Score 53.4; DB 10; Length 623; Best Local Similarity 51.1%; Pred. No. 0.082; Matches 120; Conservative 0; Mismatches 115; Indels 0;
                                                                                                            Location/Qualifiers
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Solanum tuberosum
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BG593553
                                                                                POLYA-No.
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BG593553
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/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI; Various sizes of sprouting eyes (2mm to 15mm) were taken from tubers. The tubers were incubated at 26c in the dark for 2-3 weeks prior to sprouting. The eyes were frozen in liquid nitrogen immediately upon removal from tubers."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
For clone info: please contact Research Genetics, Libraries Division tel 1-800-711-6195, email cdna@resgen.com Seq primer: M13F-R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18.1%; Score 49.4; DB 10; Length 557; llarity 71.2%; Pred. No. 0.55; Conservative 0; Mismatches 31; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89 cgtcgtcaaacagaccggccagaagcctcactacgtcggacactccatggg 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:4113"
/clone="cSTS4D6"
/tissue_type="sprouting eyes from tubers"
/dev_stage="12-14 weeks post harvest"
/lab_host="SOLR"
                                                                                                 /organism="Solanum tuberosum"
/cultivar="Kennebec"
                                                                                                                                                                                                                                                                                                                                                                                           150 t
                                                         Location/Qualifiers
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nes 79; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                           147
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Best Local Si
Matches 79;
                                                                                                                                                                                                                                                                                                                                                                                           BASE COUNT
                                                           FEATURES
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Sequence 1 Sequence 1

Appli Appli

sequence 1, A sequence 1, A sequence 1, A Sequence 6, A Sequence 6, A Sequence 15, Sequence 15,

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1652 agatectgeagggetgeeggetgteggaggagaegtaegaggeeetggagaeggeeett 1711
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  agaagcotcactacgtcggacactccatggggacgctggtggcgctggcggccttctcgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  169 agggccgggtggtgagccagctgaaatccgcggcgctgctcacgccggtggcctacctcg
                                                                                                                                                                                                                                                                                                                                                                                         US-09-105-537-40

Sequence 40, Application US/09105537A

Sequence 40, E26202

GENERAL INFORMATION:

SAPLICANT: Sherman, D.H.

APPLICANT: Xue, Y.

APPLICANT: Xue, Y.

APPLICANT: Liu, H.

TITLE OF INVENTION: DNA encoding methymycin and pikromycin

FILE REFERENCE: 600, 438US1

CURRENT PAPLICATION NUMBER: US/09/105,537A

CURRENT FILING DATE: 1998-06-26

NUMBER OF SEQ ID NOS: 43

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 40.6; DB 4; Length 2:
Pred. No. 0.057;
0; Mismatches 90; Indels
US-09-073-674-1

US-08-74-982A-1

US-08-139-134-1

US-08-139-134-1

US-08-14-130A-34

US-08-14-130A-34

US-09-773-816-1

US-09-773-816-1

US-09-773-816-1

US-09-231-818-6

US-09-231-818-6

US-09-231-818-6

US-08-920-827-15

US-08-920-827-15

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US-09-103-840A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Streptomyces venezuelae US-09-105-537-40
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1 Similarity 51.1%;
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Best Local Similarity
Matches 94; Conserv
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4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
                   GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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Maximum Match 100%
Listing first 45 summaries

    nucleic search, using sw model

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Maximum DB seq length: 2000000000
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RECOMBINANT NARBONOLIDE POLYKETIDE SYNTHASE
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/681,129
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APPLICANT: Mettenleiter, Thomas Cristoph
TITLE OF INVENTION: Pseudorabies virus vaccine
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSE: Organon Teknika Corporation
                                 CURRENT APPLICATION NUMBER: US/09/320,878A
CURRENT APPLICATION NUMBER: US/09/320,878A
CURRENT PELLING DATE: 1999-05-27
EARLIER FILING DATE: 1999-06-28
EARLIER FILING DATE: 1998-08-28
EARLIER APPLICATION NUMBER: CIP OF 09/141,908
EARLIER FILING DATE: 1998-06-06
EARLIER FILING DATE: 1999-02-08
EARLIER FILING DATE: 1999-02-08
EARLIER FILING DATE: 1999-02-08
EARLIER APPLICATION NUMBER: 60/119,139
EARLIER APPLICATION NUMBER: 60/100,880
EARLIER FILING DATE: 1998-09-22
EARLIER APPLICATION NUMBER: 60/100,880
EARLIER FILING DATE: 1998-09-22
EARLIER FILING DATE: 1998-09-38
NUMBER OF SEO ID NOS: 34
SOFTWARE: PATENTIN VET: 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: DNA
; ORGANISM: Streptomyces venezuelae
US-09-320-878-21
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Patent No. 5738854
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TITLE OF INVENTION: RECOMBIN. FILE REFERENCE: 300622002120
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Matches 94; Conserv
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MEDIUM TYPE: Diskette, 3.5 inch; 713 Kb Storage COMPUTER: IBM Compatible (Gateway 2000)
OPERATING SYSTEM: Windows 3.1
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Pred. No. 0.3;
                                                                                            EP 92.203.079.6
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APPLICANT:
GOVINGAWAMY Chinnadurai
TITLE OF INVEWION: Isolation and ch
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: G. Chinnadurai
STREET: 3681 Park Avenue
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/244,446
FILING DATE: 02-JUN-1994
CLASSIFICATION: 424
APPLICATION NUMBER: EP 92.203.075
FILING DATE: 06-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: GOrmley, Mary E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM Compatible (Gatewa:
OPERATING SYSTEM: Windows 3.1
SOFTWARE: Word for Windows (6.0)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553,99
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                                                                                                                                                                                                                                                                                   LENGTH: 1578 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                       NAME: GORMLEY, MATY E.
REGISTRATION NUMBER: 34,409
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 258-5200
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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51.5%;
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ATTORNEY/AGENT INFORMATION:
NAME: NO. 57735996
INFORMATION FOR SEQ ID NO: 1:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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STATE: Missouri
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US-08-681-129-1
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Sequence 1, Application US/08474933

Patent No. 5866410

GENERAL INFORMATION:
APPLICANT: Ryan, Michael J.
APPLICANT: Etrathy, Nancy
APPLICANT: Fantih, Susan E.
TITLE OF INVENTION: Cloung of the biosynthetic pathway for TITLE OF INVENTION: useful therein
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2255 GTCATCGACCGGGTCGGCGTCGACCGCGGGGGACACCCAGACCGACTCGCACACTC 2314
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                                      PatentIn Release #1.0, Version #1.25
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Pred. No. 0.77;
0; Mismatches 60
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STREET: One Cyanamid Plaza
CITY: Wayne
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                  31,255-02
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/125,468
FILING DATE: 22-SEP-1993
ATTORNEY/AGENT INFORMATION:
                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/125,468
FILING DATE: 22-SEP-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA: US/08/474,933 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: TSEVAGO, ESTELLE J
REGISTRATION UNDRER: 31,125
REFERENCE/DOCKET NUMBER: 31,25
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201)831-3341
TELEPAS: (201)831-3365
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; MOLECULE TYPE: DNA (genomic) US-08-125-468-1
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illarity 54.9%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 30001 base pairs TYPE: nucleic acid
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Best Local Similarity
Matches 73; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-474-933-1
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Sequence 1, Application US/08125468

Patent No. 5589385

GENERAL INFORMATION:
APPLICANT: Eyan, Michael J.
APPLICANT: Strathy, Nancy
APPLICANT: Strathy, Nancy
APPLICANT: Strathy, Nancy
APPLICANT: Cloning of the biosynthetic pathway for
TITLE OF INVENTION: Cloning of the biosynthetic pathway for
TITLE OF INVENTION: useful therein
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Cyanamid Company
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                875 GCCCTGAAGGAGGGCCGGATCCGCGGCGCGCCCTGGATGTGCACGAGTCGGAACCCTTC 934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 13.8%; Score 37.6; DB 1; Length 2085; Best Local Similarity 48.1%; Pred. No. 0.32; Matches 100; Conservative 0; Mismatches 108; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      231 cacatnaacanccccaatnggaatcctg 258
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RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                        PACT30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ute Schaeper
Janice M. Boyd
Sulekha Verma
Erik Uhlmann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T. Subramanian
G. Chinnadurai
                                                                                                                                                                                                                                                                                                                                                                                                                                      PUBLICATION INFORMATION:
                                                                                                                                                                                                                             ORGANISM: human
INDIVIDUAL ISOLATE: F
CELL TYPE: B-cell
IMMEDIATE SOURCE:
TYPE: nucleic acid
STRANDEDNESS: single
                                                           TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: no
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                                                                                                                                                                 ANTI-SENSE: no
ORIGINAL SOURCE:
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STREET: CALL
THE WAYNE
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AUTHORS: G.
TITLE: Molecton Procured Procu
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                                                                                                                                                                                                                                                                                                                                                                              LIBRARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-553-999B-1
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US-08-125-468-1
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TYPE: nucleic acid
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                 STRANDEDNESS:
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US-09-651-656-16
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LENGTH: 3283
                                                                                                                                                                                       Query Match
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APPLICANT: ST. GEORGE-HYSLOP, PETER H

APPLICANT: ROMMENS, JOHANNA M

APPLICANT: RASER, PAUL E

TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED

TITLE OF INVENTION: TO ALZHEIMER'S DISEASE AND USES THEREFOR, NUMBER OF SEQUENCES: 41

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                Score 37; DB 2; Length 30001;
Pred. No. 0.77;
0; Mismatches 60; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: LERNER, DAVID, LITTENBERG, KRUMHOLZ & MENTLIK
STREET: 600 SOUTH AVENUE WEST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SCHERING 3.0-017 CIP CIP IV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SISLE.

SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/888,077A
FILING DATE: 03-JUL-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/592,541
FILING DATE: 26-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: PALISI, THOMAS M
SCHERING
                                   31,255-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 30, Application US/08888077A Patent No. 6020143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
             REGISTRATION NUMBER: 31,145
REFERENCE/DOCKET NUMBER: 31,25
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201)831-3241
TELEPHONE: (201)831-3305
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 30001 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RECISTRATION NUMBER: 36,629
REFERENCE/DOCKET NUMBER: SCHE
TELECOMONICATION INFORMATION:
TELEPHONE: (908) 654-5000
TELEFAX: (908) 654-7866
INFORMATION FOR SEQ. ID NO: 30:
                                                                                                                                                                                                                         ; MOLECULE TYPE: DNA (genomic) US-08-474-933-1
                                                                                                                                                                                                                                                                                                  Query Match 13.6%;
Best Local Similarity 54.9%;
Matches 73; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 07090-1497
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
Tsevdos, Estelle J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
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STATE: NJ
                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
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APPLICANT: LAWRENCE LIVERMORE NATIONAL LABORATORY
TITLE OF INVENTION: DETECTION AND QUANTITATION OF SINGLE NUCLEOTIDE
TITLE OF INVENTION: DOLYMORPHISMS, DNA MISMATCHES
TITLE OF INVENTION: DNA DAMAGE AND DNA MISMATCHES
FILE REPERENCE: IL-10689
CURRENT APPLICATION NUMBER: US/09/651,656
CURRENT ELLING DATE: 2000-08-29
PRIOR APPLICATION NUMBER: 60/192,764
PRIOR FILING DATE: 2000-03-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 acgtcggacactccatggggacgctggtggcgctggcggccttctcggagggccgggtgg 180
                                                                                                                                                                                                                                                                                                                    146 ACATNGACAAGCTCCTGGGGGGCCCAGATCGGGCTGGAGGACTTCATCTTCGCCCACGTGA 205
                                                                                                                                                                                                                                                                                                                                                                   181 tgagccagctgaaatccgcgggcgctgctcacgccggtggcctacctcgnccacatnaaca 240
                                                                                                                                                                                                                                                                                                                                                                                             206 AGGGGYAGCGCAAGGAGGTGTTCAWGTCGGAGGATGYACTCGGKCTCACCATCA 265
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                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                        Score 36; DB 3; Length 404;
Pred. No. 0.59;
1; Mismatches 61; Indels
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Pred. No. 1.1;
0; Mismatches 90;
                                          ; NAME/KEY: misc_feature
; LCCATION: 1..404
; CTHER INFORMATION: /note= "Y2H35"
US-08-888-077A.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 9
US-08-390-878-17
; Sequence 17, Application US/08390878
; Patent No. 5700683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 16, Application US/09651656 Patent No. 6340566 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: DNA
; ORGANISM: Thermus thermophilus
US-09-651-656-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13.0%;
                                                                                                                                                                               13.2%;
52.7%;
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SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                       Best Local Similarity 52.7
Matches 69; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              266 CGGACAACGGG 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 nccccaatngg 251
TOPOLOGY: linear FEATURE:
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Best Local Similarity
Matches 89; Conservi
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Sequence 3, Application US/08465161; Patent No. 5500370
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                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (414) 277-5709
TELEFAX: (414) 277-5774
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 54.1%;
Matches 72; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 501 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleic acid
EDNESS: double
                      COMPUTER READABLE FORM:
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                                                                                   OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                             MEDIUM TYPE:
                                                                                                                                                                                            FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120 tacgicggacactccaiggggacgciggtggcgciggcggccttcicggagggccgggig 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 gicaacgaccigccggccaiggicgacticgicgicaaacagaccggccagaagccicac 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 15239;
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                  APPLICANT: Mahairas, Gregory G.
TITLE OF INVENTION: VIRULENCE-ATTENUATING GENETIC DELETIONS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Street Tower, 20th
STREET: Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      180 gigagecagetgaaaicegeggegetgeteaegeeggtggeetaeetegne 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85; Indels
                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/390,878
FILING DATE: 17-FEB-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Jendrisak, Jerome J.
TITLE OF INVENTION: THERMOSTABLE RIBONUCLEASE H
TITLE OF INVENTION: THEREFORE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles & Brady
STREET: 411 East Wisconsin Avenue
CITY: Milwaukee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 35.6; DE Pred. No. 1.5; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15371A-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: HUNTER, TOM
REGISTRATION NUMBER: 38,498
REGISTRATION NUMBER: 15371
TELECOMMUNICATION INFORMATION:
TELEPAN: 415/543/9607
INFORMATION FOR SEQ 1D NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 15239 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/08163181
Patent No. 5459055
Stover, Charles K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: DNA (genomic)
US-08-390-878-17
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50.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 13.0°
Best Local Similarity 50.3°
Matches 86; Conservative
                                                                                                                                                                   CITY: San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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                                                                                                                                                                                                                                         94105
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MEDIUM TERE READABLE FORM:

MEDIUM TERE. FLORPY GIST

COMPUTER: IN PROCEEDINGS

SOFTWARE: 11.251 Netabos 11.0, Version

SOFTWARE: 11.251 Netabos 11.0, Version

MEDIUM SERIES PROMATION:

MARILLOTION UNBER: US/08/163,181

FILING DATE: 2. DEC.1917

MATCHING/MATCHON DATA:

APPLICATION WHORE: US/08/163,181

FERENMENT/COMPUTER: US/08/163,181

FORMACIO: TILING COMPUTER: US/08/163,181

FORMACIO: TILING WHIGHE: US/08/163,181

FORMACIO: TILING WHIGHE: US/08/163,181

FORMACIO: TILING WHIGHE: US/08/163,181

FORMACIO: TILING WHIGHE: US/08/163,181
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GENERAL INFORMATION:
APPLICANT: Jendisak, Jerome J.
APPLICANT: Jenth, Robert E.
APPLICANT: Dahl, Gary A.
TITLE OF INVENTION: THERMOSTABLE RIBONUCLEASE H AND GENETIC CONSTRUCTS THEREFOR NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                       62 caacgacctgccggccatggtcgacttcgtcgtcaaacagaccggccagaagcctcacta 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       195 CAACCGCATGGAGCTCAAGGCGCCATAGAGGGCCTAAAGGCCCTCAAGGAGCCTTGCGA 254
                                                                                                                                                                                                                                                                                                                                Query Match 13.0%; Score 35.4; DB 1; Length 552; Best Local Similarity 54.1%; Pred. No. 0.89; Matches 72; Conservative 0; Mismatches 61; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version SOFTWARE: #1.25
CURRENT APPLICATION DATA: RAPLICATION NUMBER: US/08/465,161
FILING DATE:
                REFERENCE/DOCKET NUMBER: 31-307-9001-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 277-5709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Baker, Jean C. REGISTRATION UNBER: 9-35,433
REFERENCE/DOCKET NUMBER: 31-307-9001-1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Milwaukee
STATE: Wisconsin
COUNTRY: U.S.A.
ZIP: 3302
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATING
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/815,095
FILING DATE: 27-DEC-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: Quarles & Brady
411 East Wisconsin Avenue
                                                                                                                                                                                                                                           ; MOLECULE TYPE: Other Nucleic Acid
US-08-163-181-4
                           TELEFAX: (414) 277-5709
TELEFAX: (414) 277-5709
TELEFAX: (414) 277-5774
SEQUENCE CHARACTERISTICS:
LENGTH: 552 base pairs
TYPE: nucleic acid
STRANDEDNESS: don's'
TOPOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/08465161 Patent No. 5500370
REGISTRATION NUMBER: P-35,433
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TELEFAX: (414) 277-5774
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 552 base pairs
TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122 cgtcggacactccatggggacgctggtggcgctggcggccttctcggagggccgggtggt 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Jendrisak, Jerome J.
APPLICANT: Smith, Robert E.
APPLICANT: Dail, Gary A.
TITLE OF INVENTION: THERMOSTABLE RIBONUCLEASE H
TITLE OF INVENTION: THEREFORE
INTER OF INVENTION: THEREFORE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                  ATTORNEY AGENT INFORMATION

NAME: Baker, Jean C.

REGISTRATION NUMBER: P-35,433

REFERENCE/DOCKET NUMBER: 31-307-9001-1

TELECHOMUNICATION INFORMATION:

TELEPHONE: (414) 277-5709

TELEFAX: (414) 277-5774

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 501 base pairs

TYPE: nucleic acid

TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version SOFTWARE: #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/163,181
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APPLICATION NUMBER: US 07/815,095
FILING DATE: 27-bEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Baker, Jean C.
                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/815,095
FILING DATE: 27-DEC-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 411 East Wisconsin Avenue CITY: Milwaukee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5459055
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MOLECULE TYPE: DNA (genomic)
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illarity 54.1%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: U.S.A.
ZIP: 53202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 72; Conserv
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DB 3; Length 1977;

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Score 35.2; DB Pred. No. 1.3; 0; Mismatches
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Patent No. 6194186
GENERAL INFORMATION:
APPLICANT: Lal, Preeti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: BILLINGS, Lucy J.
REGISTRATION NUMBER: 36,749
REFRENCE/COCKET NUMBER: PF-0.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                   o;
12.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 3174 Porter Dr
CITY: Palo Alto
STATE: CA
                                   94; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                           211 cgccggtggcct 222
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                  Best Local Similarity
Matches 94; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                   US-08-977-816-2/c
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 Query Match
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                                                                                                                                                                                                                                                                                       62 caacgacctgccggccatggtcgacttcgtcgtcaaacagaccggccagaagcctcacta 121
                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Lal, Preeti
APPLICANT: Hillman, Jennifer L.
APPLICANT: Bandman, Olga
APPLICANT: Corley, Neil C.
APPLICANT: Corley, Neil C.
APPLICANT: HUMAN PROTEIN KINASE AND KINASE INHIBITORS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                      Query Match
13.0%; Score 35.4; DB 1; Length 552;
Best Local Similarity 54.1%; Pred. No. 0.89;
Matches 72; Conservative 0; Mismatches 61; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ...nrASE A....nuDRESS:
...urkSSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/231,529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PF-0429 US
                  ; TOPOLOGY: linear
; MOLECULE TYPE: Other Nucleic Acid
US-08-465-161-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/977,816
                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 14
US-09-231-529-2/c
Sequence 2, Application US/09231529
; Patent No. 6096308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNAL, CASSILLINGS, LUCY J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
ATTORNEY/AGENT INFORMATION:
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LENGTH: 1977 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
double
                                                                                                                                                                                                                                                                                                                           182 gagccagctgaaa 194
                                                                                                                                                                                                                                                                                                                                                    315 AGGCTGGCGGAAA 327
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APPLICANT: Lal, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; IMMEDIATE SOURCE:
; LIBRARY: KIDNN
; CLONE: 3453694
US-09-231-529-2
STRANDEDNESS:
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91 tcgtcaaacagaccggccagaagcctcactacgtcggacactccatggggacgctggtgg 150
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                                                                                                                                                                                                        956 TGCCCACAGGACTTGGTCCGAAGGGGCAAGAAGTTGGAGCCATCCCAGGCTGTGAGGTAG 897
                                                                                                                                                                                                                                                                                                                 896 CAGGGAGGGGGCTGGCGCAGGCGCTTGTGGGGAATTTGCACTGTGAAGAGTCGCAGGCCA 837
Gaps
                                                                               31 actggaactggtcctgggatgacctggtagtcaacgacctgccggccatggtcgacttcg 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Lal, Preeti
APPLICANT: Hillman, Jennifer L.
APPLICANT: Bandman, Olga
APPLICANT: Corley, Neil C.
APPLICANT: Corley, Neil C.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: HUMAN PROTEIN KINASE AND KINASE INHIBITORS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
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98; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/977,816
FILING DATE: Filed Herewith
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Pred. No. 1.3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PF-0429 US
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Best Local Similarity
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0;

Search completed: October 10, 2002, 03:13:24 Job time: 3582 sec

S. spinosa DNA fra Drosophila melanog Drosophila melanog S. venezuelae macr

Nucleotide sequenc Contig 002 from co Streptomyces grise Streptomyces grise

Pseudomonas putida Pseudomonas oleovo Corn sterol acyltr Corn putative leci S. aggregatum PKS Amycolatopsis medi Soybean acid triac Pimaricin biosynth Drosophila melanog

DNA encoding trypa DNA encoding novel Drosophila melanog Streptomyces sp. C Nucleotide sequenc Open reading frame Nucleotide sequenc Streptomyces sp. C Nucleotide sequenc Partial nucleotide fotal DNA sequence

Minimum DB : Maximum DB :

Database

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Result

459786

Searched:

CDNA sequence #141

aureofaciens DN Nucleotide sequenc

Corn sterol acyltr Corn putative leci Human CDNA sequenc

Streptomyces globi Streptomyces globi

OM nucleic

Run on:

Sequence:

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Triacylglycerol lipase; corn; maize; fatty acid; seed oil; vegetable oil; transgenic plant; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cahoon RE, Kinney AJ, Rafalski JA;
                                                                                                                                                                                                                                                                                                                                                                                   ALIGNMENTS
                                                         AAI71296
AAF81954
AAD07024
AAD07023
AAS01094
                                                                                                                             AAA49205
AAH18567
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AAX05110
AAA58471
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AAS01095
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AAZ34959
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ABL12741
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AAS83818
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AAF89965
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AAZ34955;
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2609.641 Million cell updates/sec
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Drosophila melanog
Rice acid triacylg
Catalpa acid triac
Drosophila melanog
Drosophila melanog
Corn acid triacylg
S. spinosa DNA fra
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                                                                                                                                                                                                                                                                                               SIDSI/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
SIDSI/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
SIDSI/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
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                                                                                                                            1 cttcctcntgcacgcttcgn.....tcctggttggccaangcgtt 273
                                                                Search time 179.61 Seconds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Description
        GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                            1736436 seqs, 858457221 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUMMARIES
                                                                 October 10, 2002, 02:14:32
                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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AAZ34958
ABL24956
AAZ34956
AAZ34952
ABL17801
ABL17801
AAZ34953
AAZ34953

    nucleic search, using sw model

                                                                                                                                              IDENTITY_NUC Gapop 10.0 , Gapext 1.0
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                                                                                                                                                                                                                   length: 0
length: 2000000000
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1718
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Match
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51.4
50.2
49.4
                                                                                                                Perfect score:
                                                                                                                                               Scoring table:
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triangly grant a portion (see AA732306) of corn acid triangly glycarol lipase (TAGL). The clone was isolated from a corn triangly glycarol lipase (TAGL). The clone was isolated from a corn leaf cDNA library. Novel acid acid explained by the corn acid catalpa, rice, soybean and wheat tissues are disclosed. The enzymes may be prepared recombinantly and used to raise antibodies, which care used for detecting the enzymes in situ in cells or in vitro in cell extracts. The polynucleotides may be used to create transgenic plants in which the TAGL levels are present at higher or lower levels than normal, or in cell types or developmental processes where they are not normally found. This would alter the level of triacylglycerol and constant of setzery lesters found in those cells. Accumulation of fatty acids with unusual structures may be desirable to eliminate expression of TAGL genes for certain applications. TAGL enzymes may also be useful for the processing of plant seed oils and for the development of novel seed clis. The TAGL enzymes can also be used as targets to facilitate the desiral as herbicides. This is desirable because inhibition of the activity of either of the enzymes could lead to an inhibition of the growth. The polynucleotides also serve as a source of probes and primers, which are useful for genetic mapping, as markers for traits in the constant of primers, which are useful for genetic mapping, as markers for traits
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 273;
                                                                                                                      This is the nucleotide sequence of the cDNA insert in clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 273 BP; 46 A; 87 C; 79 G; 54 T; 7 other;
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Pred. No. 7.8e-54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97.4%; Scur.
100.0%; Pred. No. ...
0; Mismatches
                                                                                     Claim 2; Page 43; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 273; Conservative
P-PSDB; AAY32306.
                                                   level
                                   Novel
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Novel plant triacylglycerol lipase polynucleotides used to alter the

level of the enzyme in transgenic plants

Claim 2; Page 48; 65pp; English.

Kinney AJ, Rafalski JA;

Cahoon EB, Cahoon RE, WPI; 2000-062036/05.

P-PSDB; AAY32309

(DUPO) DU PONT DE NEMOURS & CO E I.

99WO-US09280 980S-0083688

29-APR-1999; 30-APR-1998;

Location/Qualifiers 184..1416

Glycine max.

Key CDS /*tag=

W09955883-A2

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This is the nucleotide sequence of a contig assembled from the entire cDNA insert in clone $81.0k002.al and a portion of the cDNA insert in clone $81.0k002.al and a portion of the cDNA insert in clone $81.0k004.n3 encoding the entire soybean activities (TAGL) (see AAX12309). The clones were isolated from soybean developing pod and seedling (5-10 day post germination) cDNA libraries. Novel acid and neutral TAGL polypeptides (See AAX12301-17) and polynucleotides (see AAX12301-17) and polynucleotides (see AAX12301-17) and polynucleotides (see AAX12301-17) and wheat tissues are disclosed. The enzymes may be prepared recombinantly and used to raise antibodies, which care used for detecting the enzymes in situ in cells or in vitro in cell extracts. The polynucleotides may be used to create transgenic than normal, or in cell types or developmental processes where they are not normally found. This would alter the level of triacylglycerol and cholesteryl esters found in those cells. Accumulation of fatty acids with unusual structures may be desirable to eliminate expression of TAGL genes for certain applications. TAGL enzymes may also be useful for the processing of plant seed oils and for the development of novel seed oils. The TAGL enzymes can also be used as targets to facilitate the useful as herbicides. This is deasirable because inhibition of the activity of either of the enzymes could lead to an inhibition of plant carried primers, which are useful for genetic mapping, as markers for traits primers, which are useful for genetic mapping, as markers for traits.
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63.0%;
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δ d οy g à g ò g ŏ g .. 0

Gaps 83

Length 1718; Indels

Score 98.2; DB 21; Pred. No. 3e-14; 0; Mismatches 87;

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Triacylglycerol lipase; soybean; fatty acid; seed oil; vegetable oil; transgenic plant; ss.

Soybean acid triacylglycerol lipase cDNA.

AAZ34958;

AAZ34958

q ŏ

144 ctggtggcgctggcggccttctcggagggccgggtggtgagccagctgaaatccgcggcg

ò g Triacylglycerol lipase; rice; fatty acid; seed oil; vegetable oil; transgenic plant; ss.

Oryza sativa

Location/Qualifiers 32..1264

Key

Rice acid triacylglycerol lipase cDNA

(first entry)

28-FEB-2000

AAZ34956;

AAZ34956 standard; cDNA; 1483

m

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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and call-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL016176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence data for this patent did not form part of the printed cification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                204 ctgctcacgccggtggcctacctcgnccacatnaacanccccaatnggaatcctg 258
                                                                                                                                                                                                                                       Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                       Drosophila melanogaster genomic polynucleotide SEQ ID NO 26341.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 26341; 21pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Myers EW;
                                                                                                            BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Li PWD,
                                                                                                          ABL24956 standard; DNA; 2608
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2000US-0614150.
                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                       pharmaceutical; gene; ds
                                                                                                                                                                                                                                                                                     Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-656860/75.
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(ABB57737-ABB72072)
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11-JUL-2000;
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Novel plant triacylglycerol lipase polynucleotides used to alter the

of the enzyme in transgenic plants

level

Claim 2; Page 44; 65pp; English

JA;

Kinney AJ, Rafalski

Cahoon RE,

EB,

Cahoon

WPI; 2000-062036/05. P-PSDB; AAX32307

DUPO) DU PONT DE NEMOURS & CO E I.

99WO-US09280 980S-0083688

29-APR-1999; 30-APR-1998;

W09955883-A2

04-NOV-1999

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This is the nucleotide sequence of the CDNA insert in clone

"Ir72.pk0015.b2 encoding the entire rice acid triacylglycerol

Ilpace (TAGL) (see AAY23307). The clone was isolated from a rice

[lose CAA32301-17) and polynucleotides (see AAZ34950-66) from corn,

Catalpa, rice, soybean and wheat tissues are disclosed. The enzymes

CC Catalpa, rice, soybean and wheat tissues are disclosed. The enzymes

CC catalpa, rice, soybean and wheat tissues are disclosed. The enzymes

CC catalpa, rice. Soybean and wheat tissues are disclosed. The enzymes

CC catalpa, rice. Soybean and wheat tissues are disclosed. The enzymes

CC catalpa, rice and used to raise antibodies, which

are used for detecting the enzymes in situ in cells or in vitro in

cell extracts. The Problynucleotides may be used to create transgenic

plants in which the TAGL levels are present at higher or lower levels

than normal, or in cell types or developmental processes where they are

cond normally found. This would alter the level of friacylglycerol and

cholesteryl esters found in those cells. Accumulation of fatty acids

with unusual structures may be desirable to eliminate expression of TAGL

concessing of plant seed oils and for the development of novel seed

colls. The TAGL enzymes can also be used as targets to facilitate the

design and/or identification of inhibitors of those enzymes that may be

considered to feither of the enzymes could lead to an inhibition of plant

contivity of either of the enzymes can a source of probes and

contivity of either of the enzymes as a source of probes and

continued to those genes, and to isolate homologous sequences from other
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Pred. No. 0.00016;
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58.8%;
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Matches 134; Conservative
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Similarity

Query Match

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                                                                                                                                                                                                    cgtcggacactccatggggacgctggtggcgctggcggccttctcggagggccgggtggt 181
                                                                                                                                                                                                                                565 tgtgggggattcacagggaactataatgggtttggcggctttgacgatgcccgaaatagt 624
                                                                                     caacgacctgccggccatggtcgacttcgtcgtcaaacagaccggccagaagcctcacta 121
                                                                                                                                                                    505 atatgacettttageaatgetaggetatgtgtatacagteacagtecaaaattetata 564
                                       Gaps
                                                                  2 ttcctcntgcacgcttcgntttcagctctactggaactggtcctgggatgacctggtagt 61
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     DB 21; Length 1483;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Triacylglycerol lipase; fatty acid; seed oil; vegetable oil;
Score 52.8; DB 21;
Pred. No. 0.0014;
); Mismatches 116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kinney AJ, Rafalski
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Catalpa acid triacylglycerol lipase cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   level of the enzyme in transgenic plants
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 19.3%;
50.8%;
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                                     Conservative
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     Query Match
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Matches 12
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              foods. In addition, it may be desirable to eliminate expression of TAGL genes for certain applications. TAGL enzymes may also be useful for the processing of plant seed oils and for the development of novel seed oils. The TAGL enzymes can also be used as targets to facilitate the design and/or identification of inhibitrors of those enzymes that may be useful as herbicides. This is desirable because inhibition of the activity of either of the enzymes could lead to an inhibition of plant growth. The polynucleotides also serve as a source of probes and primers, which are useful for genetic mapping, as markers for traits linked to those genes, and to isolate homologous sequences from other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL161840-ABL16175) and the encoded proteins
 with unusual structures may be a positive phenotype in plants used for
                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster genomic polynucleotide SEQ ID NO 4876.
                                                                                                                                                                                                                                                                                   Length 705;
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                                                                                                                                                                                                                                                                                                                      31; Indels
                                                                                                                                                                                                                              Sequence 705 BP; 165 A; 165 C; 188 G; 181 T; 6 other;
                                                                                                                                                                                                                                                                                 Score 52; DB 21;
Pred. No. 0.0021;
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71.78;
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11-JUL-2000; 2000US-0614150.
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Best Local S
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The sequence data for this patent did not form part of the printed
The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
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                                                                                                                                                                                                                                                                                                                                                                                                                        developmental biology; cell signalling; insecticide;
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                                                                          Length 1651;
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                                                                        Score 51.4; DB 23; Length
Pred. No. 0.0031;
0; Mismatches 89; Indels
                                           Sequence 1651 BP; 307 A; 524 C; 485 G; 335 T; 0 other;
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ID ABL17800 standard; DNA; 6656 BP.
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                                                                                                129;
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                                                                            Query Match
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Matches 12
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specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                      5233 CGCTTCTGGCGATTCAGCTGGCACGAGATTGGCATCTACGACCTGCCCGCCATCGTGGAT 5174
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                                                                                                                                                                                                       9
                                                                                                                                                       Length 6656;
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                                                                            0 other;
                                                                                                                                                                                                       Indels
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                                                                            Sequence 6656 BP; 1697 A; 1581 C; 1625 G; 1753
                                                                                                                                                  Score 51.4; DB 2
Pred. No. 0.0035;
0; Mismatches 8
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                                                                                                                                                    18.8%;
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                                                                                                                                                                            Similarity
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Best Local Simil
Matches 129; C
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cell extracts. The polynucleotides may be used to raise antibodies, which are used to detect the enzymes in situ in cells or in vitro in cell extracts. The polynucleotides may be used to create transgenic plants in which the TAGL levels are present at higher or lower levels than normal, or in cell types or developmental processes where they are not normally found. This would alter the level of triacylajivecrol and cholesteryl esters found in those cells. Accumulation of fatty acids with unusual structures may be a positive phenotype in plants used for foods. In addition, it may be desirable to eliminate expression of TAGL genes for certain applications. TAGL enzymes may also be useful for the processing of plant seed oils and for the development of novel seed oils. The TAGL enzymes can also be used as targets to facilitate the cesting and/or identification of inhibitors of those enzymes that may be useful as herbicides. This is desirable because inhibition of the cuseful as herbicides. This is desirable because inhibition of plant primers, which are useful for genetic mapping, as markers for traits infect to those genes, and to isolate homologous sequences from other

Sequence 859 BP; 193 A; 213 C; 206 G; 245 T; 2 other;

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                                                                                                                        tctactctctctgttcatgataagcttttctgggattggagttggcaagaccttgctgaa 495
                                                                                                                                                             63 aacgacctgccggccatggtcgacttcgtcgtcaaacagaccggccagaagcctcactac 122
                                                                                                                                                                                       496 tacgacgttttggcaatgttaagctatgtatatacagttgcacagtccaaaattttgtat 555
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                                                                                3 tectentgeaegettegnttteagetetaetggaactggteetgggatgaeetggtagte 62
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Length 859;
Score 50.2; DB 21; Length
Pred. No. 0.0056;
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    n 18.4%;
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polyketide synthase; biosynthesis; transgenic plant; insect resistance; Salas JA; Froede R, Velten R, S. spinosa DNA fragment SEQ ID 3. Forosamine; trimethylrhamnose; spinosyn; polyketide aglycone; macrolide; insecticidal; ds. AAF88314 standard; DNA; 25360 99DE-1057268 99DE-1040596 (first entry) Saccharopolyspora spinosa Eberz G, Moehrle V, WPI; 2001-267102/28. (FARB) BAYER AG. DE19957268-A1. 29-NOV-1999; 27-AUG-1999; 28-AUG-2001 08-MAR-2001 AAF88314; AAF88314

99DE-1040596

27-AUG-1999;

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This invention describes a novel method nucleic acid (I) and its encoded polypeptide (II) containing at least one region that encodes an enzymatic activity involved in biosynthesis of spinosyns. (I) are used (I) to identify, inactivate or modulate genes involved in the biosynthesis of (II); (Ii) to generate a library of polyketide synthases; (Iii) for adding forosamine or trimethylrhamnose to a spinosyn or polyketide adjunction and (IV) for recombinant production of the corresponding enzymes, which are used for production of (II), their precursors or derivatives, including production of transgenic plants that express (II) and thus have increased resistance to insects. (I) are also useful as markers for sequencing of the Saccharopolyspora spinosa genome. (II) are also be used to raise specific antibodies, useful for identifying expression clones in a gene bank. Cells transformed with (I) may produce (II) at significantly increased levels or produce new derivatives of (II). This sequence represents a genomic DNA fragment of the S. spinosa genome which contains the coding regions for proteins involved in forces and polyketide synthase biosynthesis.
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                      enzymes for spinosyn biosynthesis, useful for insecticidal spinosyns and their derivatives
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transgenic plant; insect resistance;
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Pred. No. 0.012;
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                                                                                                                7; Page 49-58; 354pp; German.
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53.8%;
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                 New nucleic acid encoding recombinant production of
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Best Local Similarity
Matches 98; Conserv
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                                                                                                                  Claim
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27-SEP-2001
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                                                                                                                                                             This invention describes a novel method nucleic acid (I) and its encoded polypeptide (II) containing at least one region that encodes an enzymatic activity involved in biosymthesis of spinosyms. (I) are used (I) to identify, inactivate or modulate genes involved in the biosynthesis of adding forosamine or trimethylinamnose to a spinosym or polyketide allorance and (IV) for recombinant production of the corresponding enzymes, which are used for production of (II), their precursors or adjivone; and (IV) for recombinant production of (II), their precursors or derivatives, including production of (II), their precursors or derivatives, including production of (II), their precursors or adding have increased resistance to insects. (I) are also useful as markers for sequencing of the Saccharopolyspora spinosa genome. (II) are macrolides with insecticidal, but not antibacterial, activity, and can also be used to raise specific antibodies, useful for identifying expression clones in a gene bank. Cells transformed with (I) may produce (II). This sequence represents a genomic DNA fragment of the S. spinosa for process.
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                                      Salas JA;
                                                                                                                                                                                                                                                                                                                                                                                        orosamine and trimethylrhamnose biosynthesis.
                                     Velten R,
                                                                                                                                       Claim 7; Page 92-102; 354pp; German.
                                     Froede R,
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                                     Moehrle V,
                                                             WPI; 2001-267102/28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
nes 98; Conserv
            (FARB ) BAYER AG
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Matches 98;
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                                                                                                                                                                                                                                                                                                                          detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 24316; 21pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 48.8; DB Pred. No. 0.013 0; Mismatches
                                                                                                                                                                                                         Myers EW;
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                                                                                                                                                                                                         PWD,
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56.3%;
23-MAR-2001; 2001WO-US09231.
                                                         23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
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                                                                                                                                                                                                                                                                                                                          New isolated nucleic acid
genes from Drosophila and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 56.3
Matches 130; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ABB57737-ABB72072).
                                                                                                                                                                                                         Adams M,
                                                                                                                                                                                                                                                                   WPI; 2001-656860/75
                                                                                                                                               (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                                                                                                                                      interactions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200171042-A2
                                                                                                                                                                                                         Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Desosamine biosynthesis; macrolide; polyketide; methymycin; pikromycin; neomethymycin; narbomycin; polyhydroxyalkanoate monomer synthase; biopolymer; antiblotic; chemotherapeutic; immunosuppressant; asthma, chronic obstructive pulmonary disease; respiratory inflammation; hypercholesterolaemia; crop protection agent; ds.
                                                                                                                                                                                                                                                                                                                                                       detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tatcaggagttetgggacttcaccttccacgagatgggcaagtacgaccttccggccaat 1802
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 24313; 21pp + Sequence Listing; English.
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Pred. No. 0.014;
0; Mismatches
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                                                                                                                                                                                                                             Myers EW;
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                                                                                                                                                                                                                             Li PWD,
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56.3%;
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23-MAR-2001; 2001WO-US09231.
                                                              23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
                                                                                                                                                                                                                                                                                                                                                   New isolated nucleic acid genes from Drosophila and interactions -
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Matches 130; Conservative
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comprising a desosanthe biosynthetic gene cluster, a fragment or its biologically active variant, where the nucleic acid sequence is not derived from the eryc gene cluster of Saccharopolyspora erythraea or Streptomyces antibioticus. The invention also relates to a macrolide biosynthetic gene cluster, or fragments thereof. The macrolide biosynthetic gene cluster encodes proteins which synthesise methymycin, parbomycin, narbomycin, narbomycin, or combination of these compounds. Recombinant or augmented cells comprising the desosamine and/or macrolide biosynthetic gene clusters are useful for the acrolide biosynthetic gene clusters are useful for the compounds. Recombinant or augmented cells comprising the desosamine compounds are useful for synthesis of methymycin, plkromycin, narbomycin. The alternative termination of polyketide production of biologically active macrolides. The macrolide biosynthetic compounds produced by the proteins are useful for synthesis of methymycin and narbomycin. The alternative termination of polyketide synthesis may be useful to prepare novel antibiotics and copyhydroxyalkanoate (PHA) monomers. The compounds produced by the polyhydroxyalkanoate (PHA) monomers. The compounds produced by the crecombinant host cells are useful as biopolymers, e.g., in packaging or biomedical applications, to engineer PHA monomer synthases or to prepare to biomedical applications, to engineer PHA monomer synthases or to prepare communications are useful as cheart asthma, chronic obstructive pulmonary disease as well as other diseases involving respiratory inflammation, cholesterol-lowering agents or macrolide-based antibiotics which are active against a variety of organisms, e.g., bacteria, including multi-drug resistant pneumcocci and other respiratory pathogens, as well as viral parasitic pathogens, or as crop protection agents (e.g., fungicides or insecticides) via expression of polyketides in plants. Sequences AA27190-Y77197.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1652 agatectgeagggetgeeggetgteggaggagaegtaegaggeeetggagaeggeeetet 1711
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to an isolated and purified nucleic acid segment
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llarity 51.1%; Pred. No. 1.1;
Conservative 0; Mismatches 90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 15; Page 431-432; 438pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                       synthesis of methymycin and pikromycin
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P-PSDB; AAY77197.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                        Sherman DH,
                                                                                                                                 06-JAN-2000
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CDS
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Location/Qualifiers

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New recombinant pick hydroxylase gene of Streptomyces venezuelae useful for converting ketolides to antibiotics and as antibiotics and intermediates in the synthesis of compounds with pharmaceutical value
                                                                                                                                                                                                                                                                                                                                                          Narbonolide synthase; polyketide synthase gene; narbonolide polyketide; antibiotic; (12-hydroxyalse; picK; desosamine biosynthesis; desosaminyl transferase enzyme; ketolide; beta-glucosidase enzyme; picromycin biosynthesis; ss.
                                                                                                                                                                                                                                                                                                         Nucleotide sequence of ORF12 which encodes a transcriptional activator.
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51.1%; Pred. No. 1.2;
tive 0; Mismatches
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                                                                                                                                    AAA75635 standard; DNA; 5970 BP
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990S-0119139.
990S-0134990.
970S-0846247.
980S-0073538.
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1772 ccga 1775
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ashley G,
                                                                                                                                                                                           AAA75635;
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                                                                                                          AAA75635
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This is contig 002 from the recombinant cosmid pKOSO23-27 DNA sequence (see AAZ56001) which contains a Streptomyces venezuelae DNA insert. The cosmid contains open reading frames which encode the various modules of the narbonolide polyketide synthase (PKS). The invention relates to
                                                                                                                                      005;
                                                                                                                                Narbonolide polyketide synthase; PKS; cosmid pKOSO23-27; contig
ketolide; amino transferase dehydrase; hydroxylase; picromycin;
antibiotic production; narbomycin; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New recombinant DNA encoding a domain of narbonolide polyketide synthase, for production of ketolide antibiotics -
                                                                                                          Contig 002 from cosmid pKOS023-27 from Streptomyces venezuelae.
                                                                                                                                                                                                                                                                       /note= "Partial amino transferase-dehydrase"
/transl_except= (Pos:180..182, aa:Xaa)
1356..2606
/*trag= c
/product= PicK
                                                                                                                                                                                                                                                                                                                                                                                /product= transcriptional_activator
/transl_except= (Pos:4818..4820, aa:Xaa)
/note= "Xaa = unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tang L;
                                                                                                                                                                                                                                                                                                                                          /hote= "Cytochrome P450 hydroxylase"
2739..5525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ashley G, Betlach MC, Betlach M, McDaniel R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 35-37; 98pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; AAY67209, AAY67213, AAY67218.
                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                    complement (1..995)
                                                                                                                                                                                                                                                             /product- PICCIV
                          AAZ56003 standard; DNA; 5970 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (KOSA-) KOSAN BIOSCIENCES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98US-0141908.
98US-0100880.
99US-0119139.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      980S-0087080
                                                                             23-MAR-2000 (first entry)
                                                                                                                                                                                           Streptomyces venezuelae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-072618/06.
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22-SEP-1998;
08-FEB-1999;
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                                                     AAZ56003;
RESULT 15.
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Gaps

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Conservative

94;

49 Matches

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g

Similarity

Query Match Best Local S

Length 5970; Indels

DB 21;

4330 aggeccaggecggegtettecageggggecceggacaaegeeteggtegegeaggeegaae 4389 atgacctggtagtcaacgacctgccggccatggtcgacttcgtcgaaacagaccggcc 108

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cc recombinant DNA containing a coding sequence for a narbonolide PKS.

Polyketides are compounds synthesised from 2-carbon units through a series of condensations and subsequent modifications. Modulars PKSs are responsible for the production of many antibiotics including picromycin. The narbonolide PKS consists of a loading module, six extender modules, come two thiosester domains. Four proteins make up the narbonolide PKS.

CC (PLCAI, PICAII, PICAII and 2, PICAII includes the loading module come extender modules 1 and 2, PICAII includes extender module 6 and a type II thiosesterase domain. The second type II thiosesterase domain. The second type II thiosesterase domain. The second type II thiosesterase and 1 of these proteins can be isolated in recombinant form from the recombinant cosmid pKOS033-27. Narbonolide is desosaminylated in S. venezuelae to yield narbomycin, the desosaminyl transferase enzyme is crecumbinant cosmid pKOS033-27. Narbonolide is desosaminylated in S. venezuelae for this conversion, and the desosaming biosynthetic genes are also found in cosmid pKOS033-27. Narbonolide (or its derivatives) con other ketolides (particularly hybrids), which may then be converted (e.g. by other enzymes recombinantly expressed in the same hosts) to polyketide antibiotics or their intermediates. The antibiotics are useful
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Sequence 5970 BP; 806 A; 2219 C; 2142 G; 800 T; 3 other;

ö 49 atgacctggtagtcaacgacctgccggccatggtcgacttcgtcgtcaaacagaccggcc 108 0; Gaps Query Match
14.9%; Score 40.6; DB 21; Length 5970;
Best Local Similarity 51.1%; Pred. No. 1.2;
Matches 94; Conservative 0; Mismatches 90; Indels 0; ò

g

οy g

169 agggccgggtggtgagccagctgaaatccgcgggcgctgctcacgccggtggcctacctcg 228 g ò

229 ncca 232 δ 4510 ccga 4513

Search completed: October 10, 2002, 03:21:46 Job time: 4034 sec

AP003920 Oryza sat AP004015 Oryza sat AB007650 Arabidops Y14367 Drosophila AC013100 Drosophil AC003923 Drosophil AC008360 Drosophil AE003699 Drosophil

DMLIPASE3 AC013100

Oryza sat Drosophil

Drosophil

AC020487 AC020487 AC009460 AC012167 AE003463

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194672 225668 105659 50402 159455 164443

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                                                                                        1 cttcctcntgcacgcttcgn.....tcctggttggccaangcgtt 273
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     GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                         1797656 seqs, 10463268293 residues
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Maximum Match 100%
Listing first 45 summaries
                                - nucleic search, using sw model
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AL132644 Streptomy AE006003 Caulobact AF232689 Rat cytom AF389112 Rhizobium

Ralstonia Streptomy Caulobact

AE389112 BAC110278 BAC110278 BAC1059 BAC079139 AE005997 C

AL646069 AF079139

4342

35540 52606 189050

AE005997

AF333761 AB018074

11386 23656 2795

AF042276

Homo sapi

AL450350 Streptomy AL662963 Oryza sat AE005703 Caulobact

OSJN00163 AE005703 SCI8

11092 14114 229896

40442

SC10F4

10295

AE006003 AF389112 AC110278 AF333761 Rhodococc AB018074 Streptomy E59713 Process for AF042276 Pseudomon

ALIGNMENTS

AX089421 Sequence AC020115 Drosophil AC007300 Drosophil AC007300 Drosophil AK048236 Arabidops AY048236 Arabidops AY022062 Drosophil AC014022 Drosophil AC009840 Drosophil AC005591 Drosophil AC005591 Drosophil AC005591 Drosophil AC023440 Orosophil AE006503 Caulobact AL049841 Streptomy AY023440 Oryza sat AF120157 Cellulomo

AX089421 AC020115 AC007300 AE004602 AY048236 AY04834 AY04349 AY052062

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AC009840 AE003591 AE006003

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64788 1479 95597 194788 297770

117.99 117.99 117.99 117.99 117.99 118.99 118.99 118.99 118.99 118.99 118.99 118.99 118.99

SCE9 AY023440 AF120157

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AP003920 140319 bp DNA linear HTG 12-JUL-2001 Oryza sativa chromosome 8 clone OJ1789_C07, *** SEQUENCING IN PROGRESS ***, in ordered pieces.
                                                                                                                                           HTG; HTGS_PHASE2.
Orgza sativa (cultivar:Nipponbare) DNA, clone:OJ1789_C07.
Orgza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (11-JUL-2001) Takuji Sasaki, National Institute of
Agrobiological Resources, Rice Genome Research Program; Kannondai
                                                                                                                                                                                                                                                                                                Ehrhartoideae; Oryzeae; Oryzea.
1 (bases I to 140319)
Sasaki,T., Matsumoto,T. and Yamamoto,K.
Oryza sativa nipponbare(GA3) genomic DNA, chromosome 8, BAC clone:0J1789_C07
Published Only in Database (2001) In press
2 (bases I to 140319)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sasaki,T., Matsumoto,T. and Yamamoto,K. Direct Submission
                                                                                                                   AP003920.1 GI:14701606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS
TITLE
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Description

SUMMARIES

Query Match Length DB

Score

Result ٠ 9 ö

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(E-mail:tasasaki@abr_affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7468)
Tel:81-298-38-7441, Fax:81-298-38-7468)
The nuclectide sequence of this BAC clone was generated by combining Monsanto and RGP-lapan sequencing data.
NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.
* NOTE: This is a "working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.

Location/Qualifiers
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L Submitted (10-400-201) Takuji Sasaki, National Institute of
Submitted (10-400-201) Takuji Sasaki, National Institute of
Agrobiological Resources, Rice Genome Research Program; Kannondai
2-1-2, Tsukuba, Ibaraki 30-8602, Japan
C-1-2, Tsukuba, Ibaraki 30-8602, Japan
T-1-181-182-284-1841, Fax:81-298-38-7468)
The nucleotide sequence of this BAC clone was generated by
Combining Monsanto and RGP-Japan sequencing data.
NOTE: It currently consists of 1 contigs. Gaps between the contigs
are represented as runs of N. The order of the pieces is believed
to be correct as given, however the sizes of the gaps between them
are based on estimates that have provided by the submitter. This
sequence will be replaced by the finished sequence as soon as it is
available and the accession number will be preserved.
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Oryza sativa nipponbare(GA3) genomic DNA, chromosome 8, BAC clone:OJ1770_H02
Published Only in Database (2001) In press
2 (bases 1 to 170857)
Sasaki,T., Matsumoto,T. and Yamamoto,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Spermatophyta: Magnoliophyta: Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

(bases 1 to 170857)
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Pred. No. 2.3e-05;
0; Mismatches 25; Indels
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Tsukuba, Ibaraki 305-8602, Japan
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/cultivar="Nipponbare"
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                                                                                           COMMENT
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Address for correspondence: **Sos@Razusa.or.jp
Address for correspondence: **Ros@Razusa.or.jp
For the latest information on annotation of this clone, please see
http://www.kazusa.or.jp/kaos/cgi-bin/agd_graph.cgi?~*MuA2
Genes with similarity to proteins in the datubases are described
'product' or 'note' qualifiers. Genes that have no significant
protein similarity are described as 'unknown protein'.

The software programs used to predict genes include: Grail
(Informatics Group, Oak Ridge National Laboratory,
http://compbio.ornl.gov/Grail-1.3/),
GENSCAN (Chris Burge, MIT, http://CR-081.mit.edu/GENSCAN.html),
NetGene2 (S.M. Hebsgaard, et al., CBS, Technical University of
Denmark, http://www.cbs.dtu.dk/services/NetGene2/) and
SplicePredictor (Volker Brendel, Stanford University,
http://gremlin.zool.iastate.edu/cgi.bin/sp.cgi)
Genes encoding tRNAs are predicted by tRNAscan-SE
(Sean Eddy, Washington University School of Medicine, St. Louis,
http://genome.wustl.edu/eddy/tRNAscan-SE/).
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Nakamura,Y., Sato,S., Kaneko,T., Kotani,H., Asamizu,E., Miyajima,N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Db 103887 TGTCAGAGCTACTGGAACTGGTCATGGGACGACATCGTGGTCAACGACATGCCTGCAACT 103828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana (strain:Columbia) DNA, clone_lib:Mitsui Pl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana genomic DNA, chromosome 5, Pl clone:MUA22.
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Submitted (03-OCT-1997) Yasukazu Nakamura, Kazusa DNA Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21 tttcagctctactggaactggtcctgggatgacctggtagtcaacgacctgccggccatg 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Institute, Department of Plant Gene Research; 1532-3, Yana,
Kisarazu, Chiba 292-0812, Japan (E-mail:ynakamu@kazusa.or.jp,
Tel:81-438-52-3935, Fax:81-438-52-3934)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Structural analysis of Arabidopsis thaliana chromosome 5. Il Sequence features of the regions of 1,191,918 bp covered by seventeen physically assigned Pl clones DNA Res. 4 (6), 401-414 (1997)
* NOTE: This is a 'working draft' sequence.

* This sequence will be replaced

* by the flinished sequence as soon as it is available and

* the accession number will be preserved.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
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                                                                                                                                                                                                                                                                                                                                                                                                                           Score 78; DB 2; Length 170857; Pred. No. 2.3e-05;
                                                                                                                                                                                                                                                                                                                     515 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25; Indels
                                                                                                                                                                                                                                                                                      /clone="OJ1770_H02"
35890 c 35885 g 48383 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AB007650.1 GI:2564050
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Nakamura,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                  BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS
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KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
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                                                                                                                   FEATURES
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complement(19124...21115)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SRGNKLCAGRLEYSKLVDANAADPSNGPINSVHFHONAQLLLTAGLDRRLRFFGIDGK
RNTKIOSIELEDCPIRKAAFLPNGSOVIVSGRRKFFYSFDLEKAKFDKIGPLVGREEK
SLEYFEVSQDSNTIAFVGROYILLVSTRTKFLIGTLKMNGSVRSLAFSEDGKHLLSS
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GGKRKPIKTVDNLTSKIDFMKFNHDAQILAIVSTMNKNSVKLVHVPSLTVFSNMPPPN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TEKEKQKLEESELVEMKKLENIJFGSIJSPVTFGKEEEEDGSALFHVDRSAVRQPDY
EDDGDDDEELSDEENGQVVAIRKGEAAWEDEEEKQINVDIASVNRLRKLRKEENEGLI
SGSEYIARLRAHHAKLNPGTDWARPDSQIVDGESSDDDDTQDGGVDDILRTNEDLVVK
                                                                                                                                                                                                                                                                                                                                                                                               YSDLAGPEYTAKYKTLIYLAGSASAEIIADIALCPFEAVKVRVQTQPGFARGMSDGFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation-"MSLSQNAPKSKGIKREELKKQYEDVEDEEEIGSDDDLTRGKRRK
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7659...7702,7780. 8141,8504...882
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9398. .11038
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GSIJVSMVVCFIYLVATPKSNVSKASSKKKR"
This sequence may not be the entire insert of this clone. It may be shorter because we remove overlaps between neighboring submissions. The 5' clone is MAC12 and the 3' clone is F18022. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /evidence=not_experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /number=1
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                                                                                    FEATURES
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5

Gaps

83

140

197 564

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25416 bp DNA linear HTG 03-NOV-1999
, *** SEQUENCING IN PROGRESS ***, in ordered
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (03-NOV-1999) Celera Genomics, 45 West Gude Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gacttcgtcgtcaaacagaccggccagaagcct---cactacgtcggacactccatgggg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  445 GATTATGTCTTGGCAAAGACTGGACAGCAGCAGGTGCAATATGTGGGCCACTCCCAGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         141 acgctggtggcgctggcggccttctcggagggccgggtggtga---gccagctgaaatcc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          505 ACCACTGTCTATCTGGTGATGGTGTCGGAGACCCGAGTACAATGACAAGATCAAGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24 cagctctactggaactggtcctgggatgacctggtagtcaacgacctgccggccatggtc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   * NOTE: This is a 'working draft' sequence.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

Location/Qualifiers
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Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 25416)
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This sequence was identified as CDM:10213216 by the subm
For further information on this sequence you may e-mail
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
9
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 57; DB 3; Length 1211;
Pred. No. 0.28;
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88; Indels
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/db_xref="taxon:7227"
5091 c 4977 g 7542 t
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                                                                                                                           /gene="lip3"
67. .1188
/gene="lip3"
/product="lipase 3"
490. .507
                                                                                                                                                                                                                                                                                                /note="active site"
323 c 323 g
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/gene="lip3"
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Matches 134; Conservative
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HTG; HTGS_PHASE2
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/protein_id="Bab08287.1"

/db_xref="G1:9787189"

/td_sxref="G1:9787189"

/translation="mrpatagnerizerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerleggerricerlegg
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/protein_id="CAA7473.1"
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/db_xref="SPTREMBL:046108"
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YSDNYILTHRIPYSERTGESNRPAFLMHGMLSSSSDWYLMGPERSARAYMLADAG
YDVWMGNARGNTVSRAHKYMETYWOFFWNESWNEIGHYDVPAMIDYYLAKTGQQQVQV
VGHSQGTTVYLVWVSERPEYNDKIKSAHLLGPAAYMGNWKSPLTRAFAPILGQPNAIV
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[ (pases 1 to 1211)
Pistillo,D., Manzi,A., Tino,A., Boyl,P.P., Graziani,F. and Malva,C. The Drosophila melanogaster lipase homologs: a gene family with tissue and developmental specific expression

J. Mol. Biol. 276 (5), 877-885 (1998)
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Genetica e Biofisica, Via Marconi 10, 80125 Napoli, ITALY
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                            8; Length 65465;
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/organism="Drosophila melanogaster"
/strain="Canton S"
/db_xref="taxon:7227"
/clone_lib="lip3"
/dev_stage="larval"
7. .1191
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/codon_start=1
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                                                                                                                                                                                                                                                                                                                                                     0.12;
                                                                                                                                                                                                                                                                                                                         ; Score 58; DB 8
; Pred. No. 0.12;
0; Mismatches
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Drosophila melanogaster
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7. .1191
/gene="lip3"
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64.9%;
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Berkeley, CA 94720
For further information about this sequence, including its location
and relationship to other sequences, please visit our sequence
archive Web site (http://www.hgc.lbl.gov/sequence-archive.html) or
send email to drosophila@genome.lbl.gov
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This Pl was assembled from the following subclones: 1_c3 (L49194), 1_a10 (L49195), 2_h3 (L49196), 1_d1 (L49197), 2_g5 (L49198), 1_f5 (L49199), 2_b4 (L49200), 2_h7 (L49201), 1_h1 (AC000596), 3_a2 (L81432), 2_f5 (L81433), 1_c12 (L79869), 2_a7 (L79869), 2_a5 (L81431), 1_c6 (AC000593), 1_a5 (AC000593), 1_a6 (L81434), 3_g6 (L81435), 1_b10 (L81436),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AC003923 82393 bp DNA linear INV 20-JAN-1998
Drosophila melanogaster (Pl DS04219 (D36)) DNA sequence, complete
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Submitted (22-DEC-1997) Berkeley Drosophila Genome Project, MS
64121, Lawrence Berkeley National Laboratory, One Cyclotron Road,
Berkeley, CA 94720, US
Sequence submitted by:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 81393)
Celniker,S.E., Aghavani,A., Arcaina,T.T., Baxter,E., Doyle,C.M., Farfan,D.E., Flanagan,J., Houston,K.A., Hummasti,S.R., Karra,K., Mearney,L., Kim,S.H., Ko,C.L., Li,M., Lomotan,M.A., Mazda,P., Mok,M.S., Nixon,K., Paoleb,J.M., Park,S., Pfelffer,B., Punch,D., Santos,R.F., Snir,E., Stevko,V., Subramanian,S., Towne,B., Mam,K.H., Whitelaw,K.R., Yee,A., Zhang,R., Zieran,L.L. and
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Unpublished (1997)
2 (bases I to 81393)
2 Celniker,S.E., Aghavani,A., Arcaina,T.T., Baxter,E., Doyle,C.M.,
Farfan,D.E., Flanagan,J., Houston,K.A., Hummasti,S.R., Karra,K.,
Farfan,D.E., Kim,S.H., Ko,C.L., Li,M., Lomotan,M.A., Mazda,P.,
Mok,M.S., Nixon,K., Pacleb,J.M., Park,S., Pfelffer,B., Punch,D.,
Santos,R.F., Snir,E., Stevko,V., Subramanian,S., Towe,B.,
Wan,K.H., Whitelaw,K.R., Yee,A., Zhang,R., Zieran,L.L. and
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                                      23535 CAGATCTTCTGGAACTTCAGCTGGAACGAGCATGTACGACGTTCCGGCGATGAT 23476
                                                                                                                                                                                  23475 GATTATGTCTTGGCAAAGACTGGACAGCAGCTGCAATATGTGGGCCACTCCCAGGGT 23416
                                                                                                                                                                                                                                                                                                                                                          23415 ACCACTGTCTATCTGGTGATGGTGTCGGAGACCCGAGTACAATGACAAGGTCC 23356
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83
cagctctactggaactggtcctgggatgacctggtagtcaacgacctgccggccatggtc
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Lawrence Berkeley National Laboratory, MS 64-121
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ACO08360 194672 bp DNA linear INV 30-JUN-2001 Drosophila melanogaster, chromosome 3R, region 87E-87F, BAC clone BACRO6H18, complete sequence.
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Celniker.S.E., Agbayani,A., Arcaina,T.T., Baxter,E., Blazej,R.G., Butchhoff,C., Champe,M., Chavez,C., Chew,M., Clasiolka,L., Doyle,C.M., Farfan,D.E., Galle,R., George,R.A., Harris,N.L., Hoskins,R.A., Houston,K.A., Hummasti,S.R., Karra,K., Kearney,L., Kim,E., Lee,B., Lewis,S., Li,P., Lomotan,M.A., Mazda,P., Pfeiffer,B., Moshrefi,M., Nixon,K., Pacleb,J.M., Park,S., Pfeiffer,B., Poon,L., Sequeira,A., Sethi,H., Snir,E., Svirskas,R., Wan,K.H., Weinburg,T., Zhang,R., Zleran,L.L. and Rubin,G.M.
                                                                                                                                                                                                                                                                                                                                                                                                                      76093 CAGATCTTCTGGAACTTCAGCTGGAACGAGATCGCATGTACGACGTTCCGGCGATGATT 76152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76213 ACCACTGTCTATCTGGTGATGGTGTGGAGAGACCGAGTACAATGACAAGATCAAGTCC 76272
                                                                                                                                                                                                                                                                                                                                                                                                  84 gacttcgtcgtcaaacagaccggccagaagcct...cactacgtcggacactccatggggg 140
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1_d3 (L77000), 3_c5 (AC000599), 3_h2, 3_h6 (AC000600), 2_e3 (AC000598).
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                                                                                                                                                                                                                                             Score 57; DB 3; Length 82393;
Pred. No. 0.18;
0; Mismatches 88; Indels
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                                                         1. .82393
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
                                                                                                                                                /clone="Pl DS04219 (D36)"
23743 a 17464 c 17263 g 23923
                                       Location/Qualifiers
                                                                                                                /chromosome="3R"
/map="87F1-87F2"
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Drosophila melanogaster
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Best Local Similarity 58.8
Matches 134; Conservative
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AC008360/c
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Eukaryota; Metazoa; Arthropoda; Tracheata; Brachycera;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

I (bases I to 225668)
Adams, M.D., Celniker, S.E., Holt, R.A., Evans, C.A., Gocayne, J.D.,
Amanatides, P.G., Scherer, S.E., Li, P.W., Hoskins, R.A., Galle, R.F.,
George, R.A., Lewis, S.E., Richards, S., Ashburner, M., Henderson, S.N.,
Sutton, G.G., Wortman, J.R., Yandell, M.D., Zhang, O., Chen, L.X.,
Brandon, R.C., Rogers, Y.H., Blazej, R.G., Champe, M., Pfeiffer, B.D.,
Wan, K.H., Doyle, C., Baxter, B.G., Helt, G., Nolson, C.R., Gabor
Miklos, G.L., Abril, J.F., Agbayani, A., An, H.J.,
Andrews-Pfannkoch, C., Baldwin, D., Ballew, R.M., Basu, A.,
Baxendale, J., Bayraktaroglu, L., Beasley, E.M., Besson, R.Y.,
                                                                                                                                                                                                                              This sequence was assembled using end sequences from a whole genome shotpun and from subclones of this BAC and its neighboring clones. For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.berkeley.edu.
                             Submitted (02-AUG-1999) Drosophila Genome Center, Lawrence Berkeley Laboratory, MS 64-121, Berkeley, CA 94720, USA On Jun 30, 2001 this sequence version replaced 91:5706740.
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AE003699 AE002708 AE003699.2 GI:10726505
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="RPCI-98 (Roswell Park Cancer Institute Drosophila melanogaster BAC library, partial EcoRI in PBACe3.6)" 40879 g 56232 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84 gacttcgtcgtcaaacagaccggccagaagcct---cactacgtcggacactccatgggg 140
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                                                                                                             Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory, MS 64-121
Berkeley, CA 94720
                                                                                                                                                                                                                                                                                                                                                                                                                                  1. .194672
/organism="Drosophila melanogaster"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="BACR06H18 (D979)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /strain="y; cn bw sp"/db_xref="taxon:7227"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /chromosome="3R"
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Benos, P.V., Berman, B.P., Bhandari, D., Bolshakov, S., Borkova, D., Botchan, M.R., Bouck, J., Brokstein, P., Brottier, P., Burtis, K.C., Busam, D.A., Buller, H., Cadleu, E., Center, A., Chandra, J., Cherry, J.M., Cawley, S., Dankke, C., Davenport, L.B., Davies, P., de Pablos, B., Delcher, A., Deng, 2., Mays, A.D., Dew, I., Dietz, S.M., Dodson, K., Doup, L.E., Downes, M., Dugan Rocha, S., Dunkoy, B.C., Dunn, P., Durbin, K.J., Evangolista, C.C., Ferriaz, C., Ferriera, S., Fleischmann, W., Fosler, C., Gabrielian, A.E., Garell, J.H., Gu, Z., Galastr, W.M., Glasser, K., Glodek, A., Gong, F., Gorrell, J.H., Gu, Z., Guan, P., Harris, M., Harris, N.L., Harvey, D., Heiman, T.J., Howland, T.J., Hernandez, J.R., Houck, J., Mostin, D., Houston, K.A., Howland, T.J., Kanison, J.A., Ketchum, K.A., Kimmel, B.E., Kodlra, C.D., Kraft, C., Kravitz, S., Kulp, D., Lai, Z., Lasko, P., Lei, Y., Lei, Y., Levitsky, A.A., Li, J., Liang, Y., Lin, X., Mattei, B., McIntosh, T.C., McLeod, M.P., McPherson, D., Merkulov, G., Milshina, N. V., Moshrefi, A., Mount, S., Milshina, N. V., Nixon, K., Nusskern, D.R., Pacleb, J.M., Palazzolo, M., Pittman, G.S., Pan, S., Palap, J.J., Pacleb, J.M., Palazzolo, M., Pittman, G.S., Pan, S., Saunders, R.D., Scheeler, F., Shen, H., Shue, B.C., Siden-Kiamos, I., Stupski, M., Weisskern, D. Strong, R., Sun, K., Shue, B.C., Siden-Kiamos, I., Stupski, M., Weisskern, D. Scheeler, F., Shen, H., Shue, B.C., Siden-Kiamos, I., Stupski, M., Weisskern, D. Scheeler, F., Shen, H., Shue, B.C., Siden-Kiamos, I., Stupski, M., Weisskern, D. Scheeler, F., Shen, H., Shue, B.C., Strath, H., Worley, K., Sun, K., Shue, B.C., Strath, Worley, K.C., Wu, D., Yang, S., Yao, Q.A., Ye, J., Yeh, R.F., Zaveri, J.S., Zhan, M., Zhong, K., Wang, Zhong, W., Sunth, G., Bang, K., Shu, S., Shu, X., Shu, S., Shu, X., Shu, S., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    join(<14264. .14296,14382. .14587,14883. .14971,15275. .15478,
15629. .>17028)
/gene="timeout"
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join(14264. .14296,14382. .14587,14883. .14971,15275. .15478,
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BEDDELRSTV DOHR IEDDCLERLVNEPARRSKOGVITKMALOTHLIANKS EILDAKKG
RGNDRPKKDVEMEGEGEDEPREEDMGSVKRYSKRYOKROWYRTPLDVGTIR
ALIGQVDSEKYQSAIEWLQECLQDASEDTEEAVEDDGVPLLPLMENOKNAMEDGDFO
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Adams,M.D., Celniker,S.E., Gibbs,R.A., Rubin,G.M. and Venter,C.J.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (21-MAR-2000) Celera Genomics, 45 West Gude Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rockville, MD, USA
On Oct 9, 2000 this sequence version replaced gi:7299726.

    ..225668
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"

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/db_xref="FLYBASE:FBgn0038118"
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/gene="timeout"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'gene="timeout"
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|5629..17028)
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'translation-"MLLSRKEIVSLLLFLTASSAPQIISVLNASVFGNVLPLHVSYEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Db 224542 CAGATCTTCTGGAACTTCAGCTGGAACATCGCCATGTACGACGTTCCGGCGATGATT 224483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gacttcgtcgtcaaacagaccggccagaagcct---cactacgtcggacactccatgggg 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oryza sativa nipponbare(GA3) genomic DNA, chromosome 6, BAC clone:OJ1628_G11
Published Only in Database (2001) In press
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Enrhartoideae; Oryzeae; Oryzea.
1 (bass 1 to 105659)
Sasaki,T., Matsumoto,T. and Yamamoto,K.
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Oryza sativa
                                                                                                                                                                                                                                                                                                                    /db_xref="Firbass:reanonoment"
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Pred. No. 0.16;
0; Mismatches 88; Indels 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xxef="FLVBASE:FBan0008141"
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58.8%;
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KVLVALGMQPPISGMEAYWRIPIYLNSADLILRSKILAGEEVDAEPEDEAADDEDGEE
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/organism="Drosophila melanogaster"
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                                                       Lucal Laboratory and the control of the control of submitted (25-JUL-2001) Takuji Sasaki, National Institute of Agrobiological Resources, Rice Genome Research Program; Kannondai 2-1-2, Taukuba, Tbaraki 305-8602, Japan (E-mail: tsasakiénias.affrc.go.jp, URL.http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7468)

The nucleotide sequence of this BAC clone was generated by combining Monsanto and RGP-Japan sequencing data.

NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* NOTE: This is a "working draft' sequence.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.
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* the accession number will be preserved.
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Pterygota, Neoptera, Endopterygota, Diptera, Brachyoera,
Muscomorpha, Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21 tttcagctctactggaactggtcctgggatgacctggtagtcaacgacctgccggccatg 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (30-DEC-1999) Celera Genomics, 45 West Gude Drive, Rockville, MD, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 53.8; DB 2;
Pred. No. 0.66;
                    Sasaki,T., Matsumoto,T. and Yamamoto,K. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="0J1628_G11"
28723 a 24017 c 23319 g 29500 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Oryza sativa"
/cultivar="Nipponbare"
/db_xref="taxon:4530"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /chromosome="6"
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Adams, M. and Venter, J.C.
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AC020487.1 GI:6664410
HTG; HTGS_PHASE2.
fruit fly.
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65.3%;
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AC009460 159455 bp DNA linear INV 14-MAR-2001 Drosophila melanogaster, chromosome 2R, region 60B-60C, BAC clone BACR04P18, complete sequence.
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                                                                                                                        5
                                                                                                                                                                          28494 CGCTTCTGGCGATTCAGCTGGCACGAGATTGGCATCTACGACCTGCCCGCCATCGTGGGAT 28553
                                                                                                                                                                                                                                                                                                                  28614 ACCGITCICCTGGIGCIGCICTCGCAGGGCGGGGACAAIGCGCGGGITCGCCAAIGCC 28673
                                                                                                                                                                                                                          87 ttcg---tcgtcaaacagaccggccagaagcctcactacgtcggacactccatggggacg 143
                                                                                                                         Gaps
                                                                                                                                                          27 ctctactggaactggtcctgggatgacctggtagtcaacgacctgccggccatggtcgac 86
                                                                                                                                                                                                                                                           28554 TACGIGCIGGGGAGGAGGAATCGCCGCCAGCTGCACTACGTCGGGCACTCGCAGGGCACC
                                                                                                                                                                                                                                                                                             144 ctggtggcgcttggcggccttctcggagggccgggtggtgagccagctgaaatcc---gcg
                                                                                                                         .
9
                                                                                  Score 51.4; DB 2; Length 50402;
Pred. No. 2;
0; Mismatches 89; Indels 6;
                                                                                                                                                                                                                                                                                                                                                                                   28674 GCCCTGTTGGCTCCGGTGCCATTCCTCCACCTGAGCAGTCC 28717
                                                                                                                                                                                                                                                                                                                                                                 201 gegetgeteaegeeggtggeetacetegneeacatnaacaneec 244
/db_xref="taxon:7227"
11696 c 11744 g 13321 t
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                                                                                      18.8%;
57.6%;
                                                                                    Query Match 18.8%
Best Local Similarity 57.6%
Matches 129; Conservative
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Berkeley Drosophila Genome Project

FEATURES

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FEATURES

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Lawrence Berkeley National Laboratory, MS 64-121
Berkeley, CA 94720
This sequence was assembled using end sequences from a whole genome shotgun and from subclones of this BAC and its neighboring clones. For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdqp@fruitfly.berkeley.edu.

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                       Submitted (21-OCT-1999) Drosophila Genome Center, Lawrence Berkeley Laboratory, MS 64-121, Berkeley, CA 94720, USA
ON Mar 14, 2001 this sequence version replaced g1:6838820.
Sequence submitted by:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DD 149958 CGCTTCTGGCGATTCACCTGGCACTGGCATCTACGACCTGCCCGCCATCGTGGAT 149899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Db 149898 TACGTGCTGGCGAGGACGATCGCCGCCAGCTGCACTACGTCGGCCACTCGCAGGCCACC 149839
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                      Celliker, S.E., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G., Butenhoff, C., Champe, M., Chavez, C., Chew, M., Clesiolka, L., Doyle, C.M., Farfan, D.E., Galle, R., George, R.A., Harris, N.L., Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L., Kim, E., Lee, B., Lewis, S., Li, P., Lomotan, M.A., Mazda, P., Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S., Pfelffer, B., Poon, L., Sequeira, A., Sethi, H., Snir, E., Svirskas, R.R., Wan, K.H., Weinburg, T., Zhang, R., Zieran, L.L. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /chromosome="2R"
/map="608-60C"
/clone="8AKCR27M17 (D1146)"
/clone=lib="RPCI-98 (Roswell Park Cancer Institute
Drosophila melanogaster BAC library, partial EcoRI in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ttcg---tcgtcaaacagaccggccagaagcctcactacgtcggacactccatggggacg 143
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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/organism="Drosophila melanogaster"
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Pred. No. 1.7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Berkeley Drosophila Genome Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /strain="y; cn bw sp"
/db_xref="taxon:7227"
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AE003463 AE002575
AE003463.1 GI:7291737
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57.6%;
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I (bases 1 to 16443)

S Celniker; E., Adams, M.D., Kronmiller, B., Tyler, D., Wan, K.H., Agans, C.A., Gocayne, J.D., Amanatides, P.G., Brandon, R.C., Rogers, Y., An, H., Baldwin, D., Banzon, J., Beson, K.Y., Busam, D.A., Carlson, J.W., Center, A., Champe, M., Davenport, L.B., Dietz, S.M., Perriera; S., Frise, E., Galle, R.F., Gargy, N.S., George, R.A., Gonzalez, M., Houck, J., Hostin, D., Howland, T.G., Moy, M., Murphy, B., Nelson, C., Nelson, K.A., Nunoo, J., Pacleb, J., Paragas, V., Park, S., Patel, S., Pfeiffer, B., Stapleton, M., Strong, R., Stirskas, R., Tector, C., Williams, S.M., Stapleton, M., Strong, R., Stirskas, R., Tector, C., Williams, S.M., Saquencing of Drosophila chromosome 2R, region 608-60C
                         Berkeley, CA 94720
This sequence was assembled using end sequences from a whole genome routs sequence was assembled using end its neighboring clones. For further information about this BAC and its neighboring clones and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.berkeley.edu.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29353 CGCTTCTGGCGATTCAGCTGGCACGAGATTGGCATCTACGACCTGCCCGCCATCGTGGAT 29294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29293 TACGTGCTGGCGAGGACGAATCGCCGCCAGCTGCACTACGTCGGGCACTCGCAGGGCACC 29234
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                                                                                                                                                                                                                                                                                                                                                                                                                               /map="60B-60C"
/clone="BACR04PI8 (D956)"
/clone=lib="RPCI-98 (Roswell Park Cancer Institute
Drosophila melanogaster BAC library, partial ECORI in
pBACe3.6)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18.8%; Score 51.4; DB 3; Length 159455; llarity 57.6%; Pred. No. 1.7; Conservative 0; Mismatches 89; Indels 6;
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Lawrence Berkeley National Laboratory, MS 64-121
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Matches 129; Conserv
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AC012167/c
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DEFINITION
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REFERENCE AUTHORS

ACCESSION KEYWORDS SOURCE

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      Adams, M.D., Celniker, S.E., Holt, R.A., Evans, C.A., Gocayne, J.D., Amanatides, P.G., Scherer, S.E., Li, P.W., Hoskins, R.A., Galle, R.F., George, R.A., Lewis, S.E., Richards, S., Ashburner, M., Handerson, S.N., Butchon, G.G., Wortman, J.T.R., Yandell, M.D., Zhang, O., Chen, L.X., Bandon, C.G., Mortman, J.T.R., Yandell, M.D., Zhang, O., Chen, L.X., Man, K.H., Doyle, C., Baldwin, D., Ballew, R.M., Basu, A., Pfeiffer, B.D., Man, K.H., Doyle, C., Baldwin, D., Ballew, R.M., Basu, A., Burker, P.G., Champe, M., Pfeiffer, B.D., Baxendale, J., Bayraktare, E.G., Helt, G., Champe, M., Pfeiffer, B.D., Baxendale, J., Bayraktare, E.G., Helt, G., Champe, M., Pfeiffer, B.D., Baxendale, J., Bayraktare, E.G., Helt, G., Champe, M., Pfeiffer, B.D., Baxendale, J., Bayraktare, E.G., Ballew, R.M., Bascon, K.Y., Baxendale, J., Bayraktare, B., Bardwin, D., Botchan, M.R., Bouck, J., Backstein, P., Botther, P., Burtis, K.C., Botchan, M.R., Botcher, A., Chandra, I.J., Cherry, J.M., Cawley, S., Daulke, C., Deng, Z., Mays, A.D., Dew, I., Dlazz, S.M., Dodson, K., Duub, P., Durbin, K.J., Evangelista, C.C., Ferraz, C., Ferrar, S.M., Guan, P., Durbin, K.J., Evangelista, C.C., Ferraz, G., Ferrar, S.M., Guan, P., Harris, M., Glasser, K., Glodek, A., Gong, F., Garrell, J.H., Gu, Z., Guan, P., Harris, M., Huck, J., Harvey, D., Heilam, T.J., Harvey, D., Heilam, T.J., Hernandez, J.R., Huck, J., Harvey, D., Heilam, T.J., Wei, M. H., Dbeyamn, C., Jalail, M., Kalush, F., Karpen, G.H., Karte, C., Li, J., Lin, X., Lin, X., Mattei, B., McIntosh, T.C., Li, J., Li, Z., Liang, Y., Lin, X., Mattei, B., McIntosh, T.C., Mortis, J., Moshrefi, A., Nount, S.M., Moy, M., Murphy, B., Murphy, D., Mortis, J., Moshrefi, A., Welle, K., Shele, F., Shel, H., Spier, E., Spier, E., Stapleton, M., Strong, R., Sun, E., Shier, K., Sander, S., Shele, R., Shele, T., Shay, G., Shay, S., Welle, M., Weisserman, D.R., Padele, G., Welle, M., Weisserman, S., Wao, G., Shay, S., Wao, G., Shay, S., Wao, S., Shay, S., 
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Adams,M.D., Celniker,S.E., Gibbs,R.A., Rubin,G.M. and Venter,C.J.
Direct Submission
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Location/Qualifiers
1. 299975
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Gaps

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Length 25360; Indels

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Eberz,G., Moehrle,V., Froede,R., Velten,R. and Salas,J.A.
Nucleic acids which code for the enzyme activities of the spinosyn
biosynthesis
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                      Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Pseudonocardineae; Pseudonocardiaceae;
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Saccharopolyspora spinosa
Barteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Pseudonocardiaeae;
                                                                                                                                                                                                                                                                                         /organism="Saccharopolyspora spinosa"
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| 9143 c 8354 g 4031 t
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53.8%; Pred. No. 5,
... 0; Mismatches
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Patent: WO 0116303-A 6 08-MAR-2001;
                                                                                                                                                                                               Patent: WO 0116303-A 3 08-MAR-2001;
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AX089421
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Saccharopolyspora spinosa
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ilarity 53.8%;
Conservative (
                                                                       Saccharopolyspora.
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Matches 98; Conservative
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SURPKNETGYNKSAAK PAAVKNEER PPVEKEVEK RYAEVBEEETEVK PEKOKESET N
GSNPPRAKSESPEPPATTEPSQCEKTOVYDSYDENITYKMPOPAADSTTVPSKRSPSYSH
RSESSHRRDRSDYVSDHDARFURPSKESEVNKDRSLLPLPIGTLPSYGGHWARESEEA
RSESSHRRDRSDYVSDHDARMSHHMPAYNNGFNNNGORPPLSYVPYONOSVHPMRA
PYGSAGGGMNMNMSOPPORTASITGGVAAKVGSGPIDDFLEAFNETMKERERKKVD
RFRSSDRIRSRSPDQRHRFKSPMYEKDNSDNLKDKRPSRERKREHSYERHYDD
RFRSSDRIRSRSPDGRHRKSPRYEKONSDNLKDKRPSRERKREHSYERHYDD
RFRSSDRIRSRSPDGRHRKSPRYEKONSTRONLKDRYPVRRSAFRENEYDPPPPGF
SSRQPNDGSRSPGGRIKRSGHRSAAPKPGKSIDDLLAFRENEYDFRPPPPGF
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METNYGKENKAKSPSPRAGLRORAERKKNKKDRAKEKGDRQKKSSSVNRSD
SOINNSSLMNESNYKKKKKORDAERKKNKKDRAKREKGDRQKKSSSVNRSD
DNIGSPRSKLSEANSVNLSKRRIDBNILGLEDSSKRAGGSDDPREARNAI
FAARAINAITRPMFFQYIINSKDNSKRSDRARARSSDRARARSD
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                                                                                                                                                                                                                                                                  /translation="MSVHYKFKSTLNPDT1FPDGLHISVGDLKREIVQQKRLGKIDF
DLQITNAQSKEEYKDDGFLIPKNTTLIISRIPIAHPTKKGWEPPAAENAFSAAPAKQD
NFNMDLSKMQGTEEDKIQAMMQSTVDXDPKTYHRIKGQSQVGEVPASYRCNKCKKSG
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10952. .11277,11566. .11715,11776. .12069,12132. .13902)
/gene="BeDNA:LD21643"
                                                                                                                                                                                                                                                                                                                                            HWIKNCPFVGGKDQQEVKRNTGIPRSFRDKPDAAENESADFVLPAVQNQEIPEDLICG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(join(14087, 14272,14352, 14548,14615, 14708, 14769, 14954,15019, 15225,15287, 15715,15787, 16063, 16125, 19028,19082, 19353,19417, 19635,20508, 20627))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Nucleotide sequence of the Celera sequence differs
from the published sequence for this transcript."
/db_xref="FLYBASE:FBan0004012"
/db_xref="FLYBASE:FBan0004012"
/db_xref="FLYBASE:FBqn0023081"
complement(<14087. .>20627)
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0; Mismatches 89; Indels 6;
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                                                                                                                     /note="BcDNA:LD21643 gene product
                                                                                                                                                                   /db_xref="FLYBASE:FBan0003231"
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/protein_id="AAF47162.1"
/db_xref="GI:7291741"
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'db_xref-"FLYBASE:FBan0003231"
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Eberz, G., Moehrle, V., Froede, R., Velten, R. and Salas, J.A.
Nucleic acids which code for the enzyme activities of the spinosyn
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/db_xref="taxon:60894"
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Db 15837 CTCAACCTGTCACTAGCGCTGCTGGCCGTGCTGCTCAACCTGAGCGGCACC 15896 ò

Oy 243 cc 244 Db 15897 AC 15898

Search completed: October 10, 2002, 03:14:03 Job time: 3656 sec

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Soybean acid triac
Soybean acid triac
Corn acid triacylg
Rice acid triacylg
Drosophila melanog
Drosophila melanog
RGL precursor. Or
Sequence of pregas
Sequence of human
Human gastric lipa
                                                                                                                         ; Search time 23.46 Seconds
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426.114 Million cell updates/sec
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1 SSCTLRFQLYWNWSWDDLVV.....PVAYLXHXNXPNXNPGWPXR
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Result
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12 156 33.3 398 22 AAB66086 14 32.9 379 15 AAR66087 15 4 32.9 379 15 AAR66087 16 14 32.9 379 15 AAR66087 16 14 32.9 379 15 AAR66018 16 14 31.8 32.9 380 15 AAR66108 18 14 31.8 31.8 32.9 22 AAB6608 22 AA6675013 22 AAB6608 23 23 AAB6608 23 23 24 23 23 AAB6608 23 23 24 23 23 AAB6608 23 23 24 23 23 AAB6608 23 23 23 AAB6608 23 23 24 23 23 AAB6608 23 23 AAB6608 23 23 AAB6608 23 AAB6608 23 23	Human lipase prote Canine gastric lipase Drosophila melanog Drosophila melanog Drosophila melanog Human TANGO 294 ma Human TANGO 294 ma Human TANGO 294 ma Human TANGO 294 ma Human Shear stress Human shear stress Human lysosomal ac Drosophila melanog	; seed oil;
156 33.3 154 32.9 154 32.9 149 31.0 145 31.0 145 31.0 145 31.0 145 31.0 147 30.1 141 30.1 138 29.5 138 29.5 139 29.5 14 24.4 115 24.4 116 24.8 116 24.8 116 24.8 116 24.8 116 24.8 116 24.8 116 24.8 116 24.8 117 5 25.1 119 25.4 110 2	98 22 AAB66086 79 15 AAR56870 80 15 AAR56871 98 22 AAR66313 99 22 AAG67513 99 5 6 AAB61608 99 5 6 AAB71442 99 5 6 AAB66068 90 22 AAB66067 90 22 AAB66067 90 22 AAB66067 91 22 AAB66067 92 22 AAB66067 93 22 AAB66067 94 22 AAB66061 95 22 AAB66061 96 22 AAB66061 97 22 AAB66061 98 22 AAB66061 99 22 AAB66063 99 22 AAB66061 90 22 AAB66061 91 22 AAB66061 92 22 AAB66061 93 22 AAB66061 94 22 AAB66061 95 22 AAB66061 96 22 AAB6683 97 22 AAB6683 98 22 AAB66863 98 22 AAB66863 99 22 AAB66863 90 22 AAB66863 90 22 AAB66863 91 22 AAB66863 91 22 AAB66863 91 22 AAB66863 92 AAB66863 93 22 AAB66863 94 22 AAB66863 96 22 AAB66863 97 22 AAB66863 98 22 AAB66863 98 22 AAB66863 98 22 AAB66863	ase fragment. maize; fatty acid nt. iflers ed by TCN" ed by GCN" ed by ANC" ed by ANC" ed by ANG"
	2 156 33. 154 32. 154 32. 154 32. 165 33. 165 33. 165 32. 165 33. 165 33. 165 33. 165 33. 165 33. 167 30. 168 29. 168 29. 168 29. 17. 5 29. 188 29. 198 29.	AY32306 standar AY32306 standar AY32306; B-FEB-2000 (fi b-FEB-2000 (fi ciacylglycerol setable oil; t sa mays. Sc-difference lsc-difference lsc-difference lsc-difference lsc-difference lsc-difference lsc-difference lsc-difference lsc-difference lsc-difference

99WO-US09280 980S-0083688

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29-APR-1999;
                                   30-APR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY32310;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          М
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence represents a portion of corn acid triacylglycerol lipase (TAGL), as deduced from the nucleotide sequence of an isolated contact and clone (see AA234955). Novel acid and neutral TAGL polypeptides CARA32301-17) and polynucleotides (see AA234950-66) from corn, catalpa, rice, soybean and wheat tissues are disclosed. The enzymes are used for detecting the enzymes in situ in cells or in vitro in are used for detecting the enzymes in situ in cells or in vitro in cell extracts. The polynucleotides may be used to create transgenic plants in which the TAGL levels are present at higher or lower levels than normal, or in cell types or developmental processes where they are cont normally found. This would alter the level of triacylglycerol and cholesteryl esters found in those cells. Accumulation of fatty acids with unusual structures may be desirable to eliminate expression of TAGL genes for certain applications. TAGL enzymes may also be useful for the processing of plant seed oils and for the development of novel seed design and/or identification of inhibitors of those enzymes that may be useful as herbicides. This is desirable because inhibition of the activity of either of the enzymes could lead to an inhibition of plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                        plant triacylglycerol lipase polynucleotides used to alter the of the \ensuremath{\mathsf{enzyme}} in transgenic plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 SSCTLRFQLYWNWSWDDLVVNDLPAMVDFVVKQTGQKPHYVGHSMGTLVALAAFSEGRVV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Triacylglycerol lipase; soybean; fatty acid; seed oil;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97.9%; Score 458; DB 21;
llarity 100.0%; Pred. No. 3.6e-52;
Conservative 0; Mismatches 0;
                                                                                Kinney AJ, Rafalski JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 SQLKSAALLTPVAYLXHXNXPNXNPGWPXR 90
                                                        (DUPO ) DU PONT DE NEMOURS & CO E I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Soybean acid triacylglycerol lipase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sqlksaalltpvaylxhxnxpnxnpgwpxr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY32309 standard; Protein; 410 AA.
                                                                                                                                                                             5; Page 43; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         vegetable oil; transgenic plant.
           99WO-US09280
                                 980S-0083688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-FEB-2000 (first entry)
                                                                                Cahoon RE,
                                                                                                     WPI; 2000-062036/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 90; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90 AA;
                                                                                                                   N-PSDB; AAZ34955
                                 30-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oryza sativa
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                                                                                Cahoon EB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                          Novel
                                                                                                                                                    level
                                                                                                                                                                            Claim
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This sequence represents the entire soybean acid triacylglycerol lipase (TAGL), as deduced from the nucleotide sequence of isolated CDNA clones (see AAZ34958). Novel acid and neutral TAGL polypeptides (see AAZ34301-17) and polynucleotides (see AAZ34950-66) from corn, Catalpa, rice, soybean and wheat tissues are disclosed. The enzymes may be prepared recombliantly and used to raise antibodies, which are used for detecting the enzymes in situ in cells or in vitro in cell extracts. The polynucleotides may be used to create transgenic plants in which the TAGL levels are present at higher or lower levels than normal, or in cell types or developmental processes where they are not normally found. This would alter the level of triacylglycerol and chosteryl esters found in those cells. Accumulation of fatty acids with unusual structures may be a positive phenotype in plants used for foods. In addition, it may be desirable to eliminate expression of TAGL genes for certain applications. TAGL enzymes may also be useful seed oils. The TAGL enzymes can also be used as targets to facilitate the useful as herbicides. This is desirable because inhibition of the activity of either of the enzymes could lead to an inhibition of plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel plant triacylglycerol lipase polynucleotides used to alter the level of the enzyme in transgenic plants \, -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59.6%; Score 279; DB 21; Length 410; 69.4%; Pred. No. 6.6e-28; ive 12; Mismatches 10; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Triacylglycerol lipase; soybean; fatty acid; seed oil;
                                                                         Kinney AJ, Rafalski JA;
(DUPO ) DU PONT DE NEMOURS & CO E I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Soybean acid triacylglycerol lipase.
                                                                                                                                                                                                                                                                                                                                                                                       Claim 5; Page 48-49; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY32310 standard; Protein; 405 AA.
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                                                                         Cahoon EB, Cahoon RE,
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                                                                                                                                                  WPI; 2000-062036/05.
N-PSDB; AAZ34958.
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Matches 50; Conserv
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29-APR-1999;
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              W09955883-A2
                                      04-NOV-1999.
                                                                                                                                           Cahoon EB,
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                                                                                                                                                                                                                                                                                                                                                                                      foods. In addition, it may be desirable to eliminate expression of plant seed oils and for the development of novel seed oils. The TAGL enzymes may also be useful for the processing of plant seed oils and for the development of novel seed oils. The TAGL enzymes can also be used as targets to facilitate the design and/or identification of inhibitors of those enzymes that may be useful as herbicides. This is desirable because inhibition of the activity of either of the enzymes could lead to an inhibition of plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              plant triacylglycerol lipase polynucleotides used to alter the of the enzyme in transgenic plants \, \cdot \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 YWNWSWDDLVVNDLPAMVDFVVKQTGQKPHYVGHSMGTLVALAAFSEGRVVSQLKSAALL 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40.2%: Score 188; DB 21; Length 405; 40.3%; Pred. No. 5.3e-16; ive 23; Mismatches 20; Indels
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vegetable oil; transgenic plant.
                                                                                       Cahoon EB, Cahoon RE, Kinney AJ, Rafalski JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "encoded by NAC"
                                                               (DUPO ) DU PONT DE NEMOURS & CO E I.
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Misc-difference 16
                                                                                                                                                                                         Claim 5; Page 50-51; 65pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Corn acid triacylglycerol lipase.
             99WO-US09280
                                     980S-0083688
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204 spisyldhvsap 215
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                                                                                                               WPI; 2000-062036/05.
N-PSDB; AAZ34959.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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            29-APR-1999;
                                     30-APR-1998;
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Matches
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This sequence represents a substantial portion of corn acid
triacylglycerol lipase (TAGL), as deduced from the nucleotide
sequence of a contig (see AA234953) assembled from isolated leaf and
shoot cDNA clones. Novel acid and neutral TAGL polypeptides (see
AA32301-17) and polynucleotides (see AA234950-66) from corn, Catalpa,
rice, soybean and wheat tissues are disclosed. The enzymes see
are used for detecting the enzymes in situ in cells or in vitro in
are used for detecting the enzymes in situ in cells or in vitro in
cell extracts. The polynucleotides may be used to create transgenic
plants in which the TAGL levels are present at higher or lower levels
than normal, or in cell types or developmental processes where they are
not normally found. This would alter the level of triacylalycerol and
cholesteryl esters found in those cells. Accumulation of fatty acids
with unusual structures may be desirable to eliminate expression of TAGL
genes for certain applications. TAGL enzymes may also be used for
foods. In addition, it may be desirable to eliminate expression of TAGL
genes for certain applications. TAGL enzymes may also be useful for the
processing of plant seed oils and for the development of novel seed
cills. The TAGL enzymes can also be used as targets to facilitate the
useful as herbicides. This is desirable because inhibition of the
activity of either of the enzymes could lead to an inhibition of plant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 SSCTLRFQLYWNWSWDDLVVNDLPAMVDFVVKQTGQKPHYVGHSMGTLVALAAFSEGRVV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel plant triacylglycerol lipase polynucleotides used to alter the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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44.2%; Pred. No. 2.8e-15;
Live 15; Mismatches 28;
                                                                                                                                                                                                                                         Rafalski JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of the enzyme in transgenic plants
                                                                                                                                                      (DUPO ) DU PONT DE NEMOURS & CO E I.
                                                                                                                                                                                                                                         Kinney AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 5; Page 40-41; 65pp; English.
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99WO-US09280
                                                                           980S-0083688
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206 kmissaallcpisyldh 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-FEB-2000 (first entry)
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                                                                                                                                                                                                                                         Cahoon RE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                WPI; 2000-062036/05.
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Drosophila melanogaster.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel plant triacylglycerol lipase polynucleotides used to alter the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 SSCTLRFQLYWNWSWDDLVVNDLPAMVDFVVKQTGQKPHYVGHSMGTLVALAAFSEGRVV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila; developmental biology; cell signalling; insecticide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38.5%; Score 180; DB 21; Length 410; 44.2%; Pred. No. 6e-15; tive 16; Mismatches 27; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster polypeptide SEQ ID NO 41898.
                                                                                                                                                       Kinney AJ, Rafalski JA;
                                                                                                                                                                                                                                      of the enzyme in transgenic plants
                                                                                                                              (DUPO ) DU PONT DE NEMOURS & CO E I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABB71702 standard; Protein; 394 AA.
                                                                                                                                                                                                                                                             Claim 5; Page 44-45; 65pp; English
                                                                            99WO-US09280
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199 kmissaallcpisyldh 215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                       Cahoon RE,
                                                                                                                                                                               WPI; 2000-062036/05.
N-PSDB; AAZ34956.
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Matches 34: Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             410 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pharmaceutical
Oryza sativa.
                        WO9955883-A2
                                                                          29-APR-1999;
                                                 04-NOV-1999
                                                                                                                                                        Cahoon EB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                    level
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The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 FOLYWNWSWDDLVVNDLPAMYDFVVKQTGQKP-HYVGHSMGTLVALAAFSE-GRVVSQLK 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 41898; 21pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36.8%; Score 172; DB 22;
44.2%; Pred. No. 6.3e-14;
iive 18; Mismatches 23
                                                                                                                                                                                                                                                                                                                      Myers EW;
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                                                                                                                                                                                                                                                                                                                   Li PWD,
                                                                                                            23-MAR-2001; 2001WO-US09231
                                                                                                                                                                        2000US-191637P.
2000US-0614150
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186 sahllgpaaymgnmksp 202
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Best Local Similarity 44.2%
Matches 34; Conservative
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                                                                                                                                                                                                                                                                                                                      Venter JC, Adams M,
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N-PSDB; ABL15805.
                                                                                                                                                                                                                                                                (PEKE ) PE CORP NY
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WO200171042-A2
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                                                                                                                                                                     23-MAR-2000;
11-JUL-2000;
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RGL, opt. used with other lipases, are useful therapeutically (1) to facilitate absorption of ingested fats in patients deficient in endogenous gastic lipase and (2) to treat disorders caused by inadequate lipase prodn. esp. mucoviscidiosis or pancreatic exocrine deficiency. It can also be used (partic. when immobilised) for enzymatic bioconversion, e.g. hydrolysis or transesterification.
                                                                                 Rabbit gastric lipase, its precursor and their DNA - useful for treating conditions linked to gastric lipase deficiency, such as mucoviscidiosis and pancreatic exocrine insufficiency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New precursor polypeptide of defined sequence - and corresp. DNA used to transform hosts for prodn. of the polypeptide
                                                                                                                                                                                                                                                                                                                                                 Length 398;
                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                   19;
                                                                                                                                                                                                                                                                                                                                                 33.8%; Score 158; DB 14;
47.0%; Pred. No. 4.4e-12;
live 14; Mismatches 19;
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 Junien J;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAP60724 standard; Protein; 398 AA.
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/label= signal
20..398
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                                                                                                                                                    Claim 1; Fig 7; 31pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84GB-0032483.
85WO-GB00599.
86GB-0019568.
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 Blanchard C,
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                                                                                                                                                                                                                                                                                                                                                                                   31; Conservative
                                1993-161080/20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1986-182910/28.
N-PSDB; AAN60685.
                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                  398 AA;
                                                  N-PSDB; AAQ42310
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(TUBB/) TUBB R S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68 LLTPVA 73
 Benicourt C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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23-DEC-1985;
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                                                                                                                                                                                                                                                                                                     Sequence
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                                                                                                                                                                                                                                                                                    is
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                                                                                                                                                                  New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                              The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YWNWSWDDLVVNDLPAMVDFVVKQTGQKP-HYVGHSMGTLVALAAFSE-GRVVSQLKSAA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5;
                                                                                                                                                                                                                               Disclosure; SEQ ID NO 23943; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 203;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rabbit gastric lipase; RGL; pRGLN2.1; fat; bioconversion; hydrolysis; transesterification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 164; DB 2;
Pred. No. 3e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
23..398
/note= "claim 1; page 10-11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17; Mismatches
                                                                                  Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR37302 standard; Protein; 398 AA.
                                                                                  Li PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35.08;
43.28;
23-MAR-2000; 2000US-191637P
               11-JUL-2000; 2000US-0614150
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115 llapvaflghlssp 128
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                                                                               Venter JC, Adams M,
                                                                                                                WPI; 2001-656860/75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 32; Conserv
                                                (PEKE ) PE CORP NY
                                                                                                                                 N-PSDB; ABL09820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   203
                                                                                                                                                                                                   Interactions -
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Sequence

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68

AAR37302;

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AAR37302 RESULT

Protein

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Gaps

9

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Best Local Similarity
Matches 31; Conserv
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137 fwafsfdemakydlpatidfivkktgqkqlhyvghsggttigfiafstnpslakriktfy 196
                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The inventors claim a pregastric lipase protein and a gene encoding
it. Gastric lipase protein is useful for oral administration to
treat lipase deficiency, e.g. cystic fibrosis or pancreatitis.
                                          The inventors claim a DNA sequence encoding AAP60723 linked to a promoter upstream and a gene for a polypeptide downstream. Particular examples are the yeast emzyme AM6, the mammalian enzyme, gastric lipase and the mammalian lymphokine, interferon-alpha2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New gastric lipase protein, esp. of human origin – for treating lipase deficiency, and DNA sequences coding for it
                                                                                                                                                                                    5;
                                                                                                                                                        DB 7; Length 398;
                                                                                                                                                        ; Score 156; DB 7; Length 39; Pred. No. 8e-12; 13; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cystic fibrosis therapy; enzyme; lipase deficiency.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence of human pregastric lipase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
1..19
20..398
                                                                                                                                                                                                                                                                                                                                                                   AAP60658 standard; Protein; 398 AA.
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                Example; Fig 5; 60pp; English.
                                                                                                                                                      Query Match 33.3%;
Best Local Similarity 47.0%;
Matches 31; Conservative 1
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86GB-0008897.
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                                                                                                                                                                                                                                                                                                                                                                                                                          22-AUG-1991 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CELL-) CELLTECH LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1986-081634/12.
N-PSDB; AAN60566.
                                                                                                               398 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               398 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (LOWE/) LOWE P A.
                                                                                                                                                                                                                                                                                               197 alapva 202
                                                                                                                                                                                                                                                                      68 LLTPVA 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-AUG-1985;
01-JAN-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-AUG-1985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-AUG-1984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO8601532-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-MAR-1986
                                                                                                                                                                                                                                                                                                                                                                                                 AAP60658;
                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lowe PA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein
                                                                                                                                                                                                                                                                                                                                           10
                                                                                                                                                                                                                                                                                                                                           RESULT
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Length 398;

33.3%; Score 156; DB 7;

Ouery Match

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This is the amino acid sequence of the human pre-duodenal (i.e. gastric)

lipase enzyme. The sequence can be used to generate transgenic plants

producing recombinant lipase in an enzymatically acitive form.

Alternatively amino acids 20-73 or 20-73 (1-4 or 1-54 of the mature

protein, respectively) can be deleted to form the derivatives designated

delta-4 or delta-54 respectively. Plants, or their extracts, expressing

the lipases or the truncated derivatives, can be used:

(a) as pharmaceuticals or food to facilitate absorption of fat, either

in healthy subjects or in patients with inadequate levels of

abstrict/pancreatic lipase e.g. those with cystic fibrosis or exocrine

pancreatic insufficient, in the elderly or in patients undergoing medical

treatment which alters fat adsorption; (b) for performing industrial or

agricultural reactions, e.g. in processing of fats or in the dalry

industry, for hydrolysis or transesterification reactions, etc., where

the plant material may provide both enzyme and substrate. The transgenic

plants can also be used for biofuel production.
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                                                                           :| :|:|:: |||| :||:||:||| |||||| | : |||
137 fwafsfdemakydlpatidfivkktgqkqlhyvghsqgttigfiafstnpslakriktfy 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Recombinant human or canine pre-duodenal lipase prodn. in transgenic plants - useful for facilitating absorption of fat, as bio-catalysts
                       Gaps
                                                       10 YWNWSWDDLVVNDLPAMVDFVVKQTGQKP-HYVGHSMGTLVALAAFSEG-RVVSQLKSAA 67
                                                                                                                                                                                                                                                                                                                                                                                                                             food; absorption; fat; pancreatic; cystic fibrosis; exocrine; dairy; hydrolysis; trans-esterification; substrate; enzyme; biofuel; human.
                                                                                                                                                                                                                                                                                                                                                                                                              plant; recombinant; extract;
                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ٠<u>;</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lenee
47.0%; Pred. No. 8e-12;
tive 13; Mismatches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gruber V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "mature protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                            Duodenal; gastric; lipase; transgenic;
                                                                                                                                                                                                                                                                                                                                                                         Human gastric lipase protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Baudino S, Benicourt C, Cudrey C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                              AAW09383 standard; Protein; 398 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 3; Fig 5; 130pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (BIOC-) BIOCEM SA. (LJOU ) INST RECH JOUVEINAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96WO-FR00606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95FR-0004754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and for prodn. of bio-fuel
                                                                                                                                                                                                                                                                                                                                       (first entry)
                 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20..999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1996-485783/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAT58916
                                                                                                                                                                 197 alapva 202
                                                                                                                               68 LLTPVA 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9633277-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-APR-1995;
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Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to TANGO or INTERCEPT proteins and coding sequences (see AAF4512-F45136 and AAF45138-F45139 and AAB66031-B66057, AAB66064-B66083 and AAB66085). The TANGO/INTERCEPT proteins and coding sequences are useful for the treatment of neurological disorders such as central nervous system (CNS) disorders. CNS-related disorders such as central nervous system (CNS) disorders. The CNS disorders include neurological and cerebrovascular disorders. The CNS disorders include Alzheimer's disease, senile dementia, Huntington's disease, amyotrophic lateral sclerosis, parkinson's, Gillse de la Tourette's syndrome, autonomic function disorders such as hypertension and sleep disorders, neuropsychiatric disorders psychoactive substance use disorders, and bipolar affective disorder. The present sequence is a sequence used in a sequence homology alignment with the TANGO/INTERCEPT.
                                                                                                 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gene therapy; TANGO protein; INTERCEPT protein; neurological disorder; central nervous system; focal brain disorder; bipolar affective disorder; global-diffuse cerebral disorder; cerebrovascular; Alzheimer's disease; senile dementia; Huntington's disease; amyotrophic lateral sclerosis; Parkinson's; Gilles de la Tourette's syndrome; hypertension; sleep; neuropsychiatric; psychoactive substance use; anxiety.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TANGO and INTERCEPT nucleic acids, proteins, and antibodies, useful for screening assays and diagnostic assays and for the treatment of neurological diseases such as Alzheimer's, Parkinson's and Huntington's
                                                                                                                                                            :| :|:|: |||| :||:|| ||| ||| ||| || || : ::|:
137 fwafsfdemakydlpatidfivkktgqkqlhyvghsqgttigfiafstnpslakriktfy 196
                                                                                               Gaps
                                                                                                                                     10 YWNWSWDDLVVNDLPAMYDFVVKQTGQKP-HYVGHSMGTLVALAAFSEG-RVVSQLKSAA 67
                                                                                                 5;
                                                          DB 17; Length 398;
                                                        33.3%; Score 156; DB 17; Length 3 47.0%; Pred. No. 8e-12; Live 13; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Barnes TM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sharp JD,
                                                                                                                                                                                                                                                                                                                                                             AAB66086 standard; Protein; 398 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 6; 359pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MILL-) MILLENNIUM PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-MAY-2000; 2000WO-US14858.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0333159.
                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                        Best Local Similarity 47.0
Matches 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          McCarthy SA, Fraser CC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human lipase protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-032313/04.
398 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      398 AA;
                                                                                                                                                                                                                                                       197 alapva 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200077239-A2.
                                                                                                                                                                                                                  68 LLTPVA 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                            30-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-DEC-2000.
                                                                                                                                                                                                                                                                                                                                                                                                     AAB66086;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
Sequence
                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     disease
                                                                                                                                                                                                                                                                                                                                             AAB66086
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137 fwafsfdemakydlpatidfivktgqkqlhyvghsqgttigfiafstnpslakriktfy 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                          10 YWNWSWDDLVVNDLPAMVDFVVKQTGQKP-HYVGHSMGTLVALAAFSEG-RVVSQLKSAA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CGL is used to improve absorption of ingested fat, in healthy and sick patients (e.g. having altered levels of gastric lipase); to treat conditions associated with insufficiency (or lack) of lipases, esp. mucoviscidosis or exocrine pencreatic insufficiency and partic. where immobilised, for bloconversions, e.g. hydrolysis or transesterification (other mammalian gastric lipases, or derivs., can be used in this application).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 YWNWSWDDLVVNDLPAMVDFVVKQTGQ-KPHYVGHSMGTLVALAAFSEG-RVVSQLKSAA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequence given below is the sequence of figure 9A, altered according to the amendments described on page 2 of the appended
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Canine gastric lipase; CGL; dog; fat; mucoviscidosis; enzyme; bloconversion; exocrine pancreatic insufficiency.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32.9%; Score 154; DB 15; Length 379; 45.5%; Pred. No. 1.4e-11; Live 15; Mismatches 19; Indels
                          Length 398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Recombinant canine gastric lipase and nucleic acid en are used for improving absorption of ingested fat, tr mucoviscidosis etc. and in enzymatic bio-conversions
Score 156; DB 22; Pred. No. 8e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Blanchard C, Junien J;
                                                                                                                                                                                                                                                                                                                                                                                                           AAR56870 standard; Protein; 379 AA.
                                                                          13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 13; Fig 9A; 52pp; French
                       33.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92FR-0015201.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-FEB-1995 (first entry)
                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Canine gastric lipase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1994-217890/26.
                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 30; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          379 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Canis familiaris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAQ68388
                                                                                                                                                                                                                                                                               197 alapva 202
                                                                                                                                                                                                                            68 LLTPVA 73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-DEC-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9413816-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR56870;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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AAR56871
                                                           RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         lipase enzyme. The sequence can be used to generate transpend plants producing recombinant lipase in an enzymatically active form.

Alternatively the first 4 or 54 amino acids of this sequence can be deleted to form the derivatives designated delta-4 or delta-54 respectively. Plants, or their extracts, expressing the lipases or the truncated derivatives, can be used: (a) as pharmaccuticals or food to facilitate absorption of fat, either in healthy subjects or in patients with inadequate levels of gastric/pencreatic lipase e.g. those with cystic fibrosis or exorcine pencreatic insufficient, in the elderly or in treatment which alters fat adsorption; (b) for performing industrial or agricultural reactions, e.g. in processing of fats or in the dairy industry, for Mydrlysis or transseterification reactions, etc., where the plant material may provide both enzyme and substrate. The transgenic plants can also be used for biofuel production.
                                                                                                                                                                                                                                                                                   Dog; duodenal; gastric; lipase; transgenic; plant; recombinant; extract; food; absorption; fat; pancreatic; cystic fibrosis; exocrine; dairy; hydrolysis; trans-esterification; substrate; enzyme; biofuel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This is the amino acid sequence of the dog pre-duodenal (i.e. gastric)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Recombinant human or canine pre-duodenal lipase prodn. in transgenic plants - useful for facilitating absorption of fat, as bio-catalysts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gruber V, Lenee P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Baudino S, Benicourt C, Cudrey C,
                                                                                                                                                                                                                                                 gastric lipase protein sequence.
                                                                                                                                  AAW09382 standard; Protein; 379 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 2; Fig 2; 130pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (LJOU ) INST RECH JOUVEINAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96WO-FR00606
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                                                                                                                                                                                                            19-AUG-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and for prodn. of bio-fuel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1996-485783/48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (BIOC-) BIOCEM SA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   379 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAT58915.
                                                                                                                                                                                                                                                                                                                                                                Canis familiaris
                                     178 alapva 183
68 LLTPVA 73
                                                                                                                                                                                                                                                                                                                                                                                                    WO9633277-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-APR-1995;
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                                                                                                                                                                      AAW09382:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Merot B;
                                                                                               14
                                                                                                              AAW09382
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Recombinant canine gastric lipase and nucleic acid encoding it are used for improving absorption of ingested fat, treating mucoviscidosis etc. and in enzymatic bio-conversions

Claim 14; Fig 9A; 52pp; French.

Blanchard C, Junien J;

Benicourt C,

WPI; 1994-217890/26. N-PSDB; AAQ68389.

(LJOU) INST RECH JOUVEINAL

93WO-FR01260.

16-DEC-1993; 16-DEC-1992;

23-JUN-1994

Canine gastric lipase; CGL; dog; fat; mucoviscidosis; enzyme; bioconversion; exocrine pancreatic insufficiency.

Canis familiaris.

WO9413816-A.

Canine gastric lipase (Met-CGL).

(first entry)

20-FEB-1995

AAR56871;

AAR56871 standard; Protein; 380 AA.

178 alapva 183

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119 fwafsfdemakydlpatidfilkktgqdklhyvghsggttigfiafstnpklakriktfy 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 YWNWSWDDLVVNDLPAMVDFVVKQTGQ-KPHYVGHSMGTLVALAAFSEG-RVVSQLKSAA 67
                                                                                           GGL is used to improve absorption of ingested fat, in healthy and sick patients (e.g. having altered levels of gastric lipase); to treat conditions associated with insufficiency (or lack) of lipases, esp. mucoviscidosis or exocrine pancreatic insufficiency and partic. where immobilised, for bioconversions, e.g. hydrolysis or transesterification (other mammalian gastric lipases, or derivs, can be used in this application).
The sequence given below is the sequence of figure 9A, altered according to the amendments described on page 2 of the appended
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 380;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32.9%; Score 154; DB 15; 45.5%; Pred. No. 1.4e-11; tive 15; Mismatches 19;
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Best Local Similarity 45.5
Matches 30; Conservative
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Search completed: October 10, 2002, 02:10:27

Job time: 1300 sec

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32.9%; Score 154; DB 17; Length 379; 45.5%; Pred. No. 1.4e-11; tive 15; Mismatches 19; Indels

Conservative

Query Match Best Local Similarity Matches 30; Conserv

68 LLTPVA 73

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09d705
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09d6cs
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                                                                                                                                                         562222
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                        562222 seqs, 172994929 residues
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                                               October 10, 2002, 02:09:57
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Q9W195
Q9D6N8
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09D766
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Q9D6T5
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Q9D6L1
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sp_invertebrate:*
sp_mammal:*
sp_mbc:*
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8 L S E E		Q95x33 caenorhabdi Q0186 caenorhabdi Q961g2 homo saplen Q96xt2 drosophila Q16529 homo saplen Q96ejQ homo saplen Q9fmt3 arabidopsis Q9fmt3 arabidopsis	0920m5 mus musculu 0920m5 mus musculu 017219 bombyx mori 01776 caenorhabdi 09425 caenorhabdi 099495 drosophila 099498 drosophila
	5 Q2V/96 5 Q20449 5 Q16956 5 Q9VFE9 5 Q9VG46	5 095833 6 09666 5 098872 5 098872 4 096620 10 096870 5 098885	
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STRAIN-CV. COLUMBIA;
MEDLINE-20083487; Pubbled-10617197;
Lin X., Raul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Lin X., Raul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
Gronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,
Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
Copenhaver G.P., Preuss D., Nierman W.C., White O., Elsen J.A.,
Salzberg S.L., Fraser C.M., Venter J.C.;
Fagure C. M., Venter J.C.;
Lindan analysis of chromosome 2 of the plant Arabidopsis
                                                                                                                                                                                     Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AC006298; AAD25569.1; -.
InterPro; IPR000379; Est_lip_thioest_actsite.
InterPro; IPR000734; Lipase.
PROSITE; PS00120; LIPASE_SER; 1.
SEQUENCE 344 AA; 38868 MW; 7BC4ED067E3602C4 CRC64;
                                       01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
PUTATIVE LYSOSOWAL ACID LIPASE.
                                     344 AA
                                                                                                                                                                     Arabidopsis thaliana (Mouse-ear cress).
                                     PRT;
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                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-CV. COLUMBIA;
                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A
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RESULT
09SKL5
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IPRO00734; Lipase

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PROSITE; PS00120; LIPASE_SER; 1.
SEQUENCE 203 AA; 22264 MW; 734E07401E85B32F CRC64;
InterPro;
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0
                Length 344;
            ; Score 170; DB 10;
; Pred. No. 1.2e-11;
17; Mismatches 27;
                                                                                                                                                                                                                                                                                 203 AA.
                                                                                                                                                                                                                                                                                 PRT;
                36.3%;
38.9%;
                                                 Conservative
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                                                                                                                                                        70 TPVAYLXHXNXP 81
                Query Match
Best Local Similarity
Matches 28; Conserv
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Q9W195;
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REALLY STRAIN-CS7BL/G3; TISSUB-TONGUE;

REDLINE-21085660; PubMed-11217851;

REALLY Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishil Y.,

RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

A Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Aizawa K., Isawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Aizawa K., Isawa M., Nishi K., Shburner M., Batalov S., Casavant T.,

RA Gottim L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Anno H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

R Browstein M.J., Bult C., Fletcher C., Fullita M., Gariboldi M.,

R Browstein M.J., Bult C., Fletcher C., Fullita M., Mombaerts P.,

R Browstein M.J., Bult C., Reshima J., Mazzarelli J., Mombaerts P.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Sasaki H., Sato K., Schoenbach C., Waltitaker C., Willming L.,

RA Wynshaw-Bootis A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

RA Wynshaw-Bootis A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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                                                                               Gaps
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                                                                                                                                                      10 YWNWSWDDLVVNDLPAMVDFVVKQTGQKP-HYVGHSMGTLVALAAFSE-GRVVSQLKSAA 67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2001 (TIEMBLIEL. 17, Created)
01-JUN-2001 (TIEMBLIEL. 17, Last sequence update)
01-DEC-2001 (TIEMBLIEL. 19, Last annotation update)
01-DEC-2001 (TIEMBLIEL. 19, Last annotation update)
01-DEC-2010 (TIEMBLIEL. 19, Last annotation update)
CLONE: 2310074E21, FULL INSERT SEQUENCE.
2310051B21RIK.
   Length 203;
                                                                           Indels
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PROSITE; PS00120; LIPASE_SER; 1.
SEQUENCE 395 AA; 44761 MW; 13889361DC8F17B9 CRC64;
Query Match 35.0%; Score 164; DB 5; Lu Best Local Similarity 43.2%; Pred. No. 3.2e-11; Matches 32; Conservative 17; Mismatches 23;
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MGD; MGI:1914967; 2310051B21Rik.
InterPro; IPR000073; Abhydrolase.
InterPro; IPR000379; Est_lip_thioest_actsite.
InterPro; IPR000734; Lipase.
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Best Local Similarity 41.9%;
watches 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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68 LLTPVAYLXHXNXP 81
2310051B21RIK PROTEIN
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                                                                                                                      SEQUENCE FROM N.A.
                                                                                     NCBI_TaxID=10090;
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Q9D796;
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RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Arawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Atawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazali Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Raoliwa H.,
RA Schriml L.M., Staubil F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fleccher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N. H.,
RA Lyons P., Marchionni L., Mashima J., Mazarelli J., Mombaerts P.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Hayshizaki Y.,
RA H
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136 FWAFSFDEMAKYDLPATIDFIVQKTGQEKIHYVGHSQGTTIGFIAFSTNPALAKKIKRFY 195
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                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ch 33.1%; Score 155; DB 11; Length 395; L Similarity 41.9%; Pred. No. 7.9e-10; 31; Conservative 15; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfan; PF00561; abhydrolase; 1.
PROSITE; PS00120; LIPASE_SER; 1.
SEQUENCE 395 AA; 44748 MW; 3ED43992458DE058 CRC64;
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Last annotation update)
                                                                                                                                                                                           (TrEMBLrel. 17, Last sequence update) (TrEMBLrel. 19, Last annotation update)
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InterPro; IPR000073; Abhydrolase.
InterPro; IPR0000779; Est_lip_thioest_actsite.
InterPro; IPR000734; Lipase.
                                                                                                                                         395 AA.
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                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-TONGUE;
MEDLINE-21085660; Pubmed-11217851;
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196 ALAPVATVKYTESP 209
                                                196 ALTPVATVKYTESP 209
              81
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                                                                                                                                                                                                                            2310051B21RIK PROTEIN.
                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
              68 LLTPVAYLXHXNXP
                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
                                                                                                                                                                                                                                                2310051B21RIK.
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01-JUN-2001
01-DEC-2001
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Q9D7C5
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STRAINCSTRUCH TISSUE-TONGUE;

XA KWAN J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

XA Arakawa T., Jara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

A Azawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Aizawa K., Isawa M., Nishi K., Kiyosawa H., Kashou T., Salto T.,

RA Aizawa K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Rochiml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

R Browstein M.J., Bult C., Fletcher C., Fullta M., Gariboldi M.,

R Browstein M.J., Bult C., Fletcher C., Fullta M., Manbaerts P.,

R Browstein M.J., Bult C., Reshoen M., Hume D.A., Kamiya M., Lee N. H.,

RA Mordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

R Winshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

R Winshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

R Winshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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MEDLINE=21085660; Pubmed=11217851;
Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Functional annotation of a full-length mouse cDNA collection.";
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PROSITE; PS00120; LIPASE_SER; 1.
SEQUENCE 395 AA; 44603 MW; D3FDBB6FEA671E3E CRC64;
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Last annotation update)
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Pred. No. 7.9e-10;
... wicmatches 26;
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MGD; MGI:1914967; 2310051B21Rik.
InterPro; IPR000073; Abhydrolase.
InterPro; IPR000379; Est_lip_thioest_actsite.
InterPro; IPR000734; Lipase.
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41.9%; Pred. No. 7.9e
tive 15; Mismatches
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Best Local Similarity 41.99
Matches 31; Conservative
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196 ALAPVATVKYTESP 209
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us-09-699-652-12.rspt

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Mus musculus (Mouse).
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                                  Hayashizaki Y.;
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RC STRAIN=C57BL/6J; TISSUE=TONGUE;

RX MEDIARE-210B5660; PubMed-11217851;

RA Arakawa T., Hara A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Arawa Y., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Saito T., Okazaki Y., Gojobori T., Bono H., Rasukawa T., Saito R.,

RA Saito T., Okazaki Y., Gojobori T., Bono H., Rasukawa T., Saito R.,

RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Saxai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Brownstein M.J., Bult C., Fletcher C., Fulita M., Gariboldi M.,

RA Mordone P., Ring B., Kingwald M., Rodriguez I., Sakamoto N.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Sasaki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
Radto T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Relot P., Lewis S., Matsuo Y., Mikaido I., Pesole G., Cuackenbush J.,
Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
Blownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
Gustincich S., Hill D., Hefmann M., Hume D.A., Kamiya M., Lee N.H.,
Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
A Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
M. Wynshaw-Bonis A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                       "Functional annotation of a full-length mouse cDNA collection.";
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EMBL: AK009437; BAB26287.1; -

MGD: MGI:1914967; 2310051B21Rik.

InterPro; IPR000073; Abhydrolase.

InterPro; IPR000734; Lipase.

Pfam; PF00561; Lipase.

Pfam; PF00561; Lipase.

PROSITE: PS000120; Lipase.

SEQUENCE 395 AA; 44684 MW; E9FB6AE85A81257F CRC64;
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Last annotation update)
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41.9%; Pred. No. 7.9e-10;
tive 15; Mismatches 26;
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01-JUN-2001 (TrEMBLEEL 17,
01-DEC-2001 (TrEMBLEEL 19,
2310051B21RIK PROTEIN.
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Best Local Similarity
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Arakawa T., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Ra Saito T., Okazaki Y., Gojobori T., Bono H., Rasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kuchi P., Lewis S., Matsuo Y., Mikaldo I., Pesole G., Quackenbush J.,
RA Sakai K., Okido T., Furuno M., Anon H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Garlboldi M.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-Oka K., Wang K.H., Weltz C., Whittaker C., Willming L.,
Rynshaw-Booris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                        "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
EMBL; AK009537; BAB26346.1; -.
MGD; MGI:1914967; 2310051B21Rik.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 395;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33.1%; Score 155; DB 11; Length 3(41.9%; Pred. No. 7.9e-10;
ive 15; Mismatches 26; Indels
                                                                                                                                                                                               InterPro; IPR000073; Abhydrolase.
InterPro; IPR000073; Est_lip_thioest_actsite.
InterPro; IPR000734; Lipase.
Pfam; PF00561; abhydrolase; 1.
PROSITE; PS00120; Lipase.SER; 1.
SEQUENCE 395 AA; 44607 MW; E43317C2254FABFB CRC64;
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PROSITE; PS00120; LIPASE_SER; 1.
SEQUENCE 395 AA; 44648 MW; CC69875653AA7A74 CRC64;
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Last annotation update)
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EMBL; AK009544; BAB26350.1;

MGD; MGI:1914967; 2310051B21Rik.

InterPro; IPR0000773; Abbydrolase.

InterPro; IPR000379; Est_lip_thioest_actsite.
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STRAIN=C57BL/6J; TISSUE=TONGUE;
MEDLINE=21085660; PubMed=11217851;
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Best Local Similarity 41.98
Matches 31; Conservative
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RESULT 10
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136 FWAFSFDEMAKYDLPATIDFIVQKTGQEKIHYVGHSQGTTIGFIAFSTNPALAKKIKRFY. 195
                               Gaps
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                                                        10 YWNWSWDDLVVNDLPAMVDFVVKQTGQ-KPHYVGHSMGTLVALAAFSEG-RVVSQLKSAA 67
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                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
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   Length 395;
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PROSITE; PS00120; LIPASE_SER; 1.
SEQUENCE 395 AA; 44685 MW; FEF96B65EA670BEE CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
33.1%; Score 155; DB 11;
41.9%; Pred. No. 7.9e-10;
iive 15; Mismatches 26;
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EMBL; AK009560; BAB26359.1;

MGD; MGI:1914967; 2310031B21Rik.

InterPro; IPR000073; Abhydrolase.

InterPro; IPR000379; Est_lip_thioest_actsite.

InterPro; IPR000734; Lipase.
                                                                                                                                                                                                                 395 AA.
                                                                                                                                                                                                                 PRT;
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MEDLINE-21085660; Pubmed-11217851;
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Mammalia; Eutheria; Rodentia;
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Best Local Similarity 41.99
Matches 31; Conservative
             Local Similarity 41.99 tes 31; Conservative
                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                           196 ALAPVATVKYTESP 209
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                                                                                                              68 LLTPVAYLXHXNXP 81
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                                                                                                                                                                                                                                                                                          2310051B21RIK PROTEIN
                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
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01-JUN-2001
 Query Match
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Matches
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STRAINCSTBL/63; TISSUB-TONGUE;

X KWAN JO. Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

X KWAN J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

X Arawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

A Lizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

X Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

X Kadota K., Matsuda H.A., Shaburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Shaburner M., Batalov S., Casavant T.,

X Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Rochiml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washlo T.,

Sakai K., Okido T., Furuno M., Anon H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

R Dronstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

R Dronstein M.J., Bult C., Fletcher C., Ramiya M., Lee N.H.,

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

R Winshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Nanachizaki V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
ADULT MALE TONGUE CDNA, RIKEN FULL-LENGTH ENRICHED LIBRARY,
CLONE: 23100161A13, FULL INSERT SEQUENCE.
MUS musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Functional annotation of a full-length mouse cDNA collection.";
Mature 409:685-690(2001).
EMBL; AR009875; BAB2655.1; ...
MGD; MGI:1914967; 2310051B21Rik.
InterPro: IPR000073; Abhydrolase.
InterPro: IPR000073; Abhydrolase.
InterPro: IPR000779; ESL_lip_thloest_actsite.
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PROSITE; PS00120; LIPASE_SER; 1.
SEQUENCE 395 AA; 44665 MW; 40CA6B67859A8C5B CRC64;
                                                       (TrEMBLrel. 17, Created)
(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
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; Pred. No. 7.9e-10;
15; Mismatches 26;
395 AA.
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01-JUN-2001 (TrEMBLrel. 17, Last seq
01-DEC-2001 (TrEMBLrel. 19, Last ann
   PRT;
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41.9%;
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PRELIMINARY;
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196 ALAPVATVKYTESP 209
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                                                                                                                                                  2310051B21RIK PROTEIN
2310051B21RIK.
                                                                                                                                                                                                            Mus musculus (Mouse).
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
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01-JUN-2001
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Q9D6T5;
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SEQUENCE FROM N.A.
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     A Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Alazawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Adota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Richell P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Brans G., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Whynaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Havachi, P., V.
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136 FWAESFDEMAKYDLPATIDFIVQKTGQEKIHYVGHSQGTTIGFIAFSTNPALAKKIKRFY 195
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MEDLINE=21085660; PubMed=11217851;
Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishli Y.,
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Salito T., Okazaki Y., Gojobori T., Bono H., Ksukawa T., Salto R.,
Kadota K., Matsuda H.A., Ashburner M., Batalow S., Casavant T.,
**Pleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
  Mammalia; Eutheria; Rodentía; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
NCBI_TaxID=10090;
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"Functional annotation of a full-length mouse cDNA collection.";
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CLOME: JAILE TONGUE CDNA, RIKEN FULL-LENGTH ENRICHED LIBRARY,
CLOME: JAI0063R07, FULL INSERT SEQUENCE.
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EMBL, AK009990; BABZ6629.1; ...

MGD; MGI:1914967; 2310051B21Rik.

InterPro; IPR0000379; ESt_lip_thioest_actsite.

InterPro; IPR000734; Lipase.

Pfam: PF00561; abhydrolase; 1.

PROSTIE: PS00120; LIPASE_SER; 1.

SEQUENCE 395 AA; 44623 MW; D3F96DB83161C3EF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33.1%; Score 155; DB 11;
41.9%; Pred. No. 7.9e-10;
ative 15; Mismatches 26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2001 (TrEMBLrel. 17, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                  STRAIN-C57BL/6J; TISSUE-TONGUE; MEDLINE-21085660; PubMed-11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        196 ALAPVATVKYTESP 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68 LLTPVAYLXHXNXP 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9D6S5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 12
Q9D6S5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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RC STRAIN-C57BL/G1, TISSUE-TONGUE;

RX MEDLINE-21085660; PubMed=11217851;

R KAWai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

R Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

R Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Arawawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Salto T., Okazaki Y., Golobori T., Bono H., Kashwawa T., Salto R.,

RA Acdta K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Rechi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quadkenbush J.,

RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

RA Hayashizaki Y.,
Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bolunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchlonni L., Maschima M., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wanshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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136 FWAFSFDEMAKYDLPATIDFIVQKTGQEKIHYVGHSQGTTIGFIAFSTNPALAKKIKRFY 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 YWNWSWDDLVVNDLPAMVDFVVKQTGQ-KPHYVGHSMGTLVALAAFSEG-RVVSQLKSAA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Wakaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi; Muridae, Murinae, Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
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09D6Q6;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
ADULT MALE TONGUE CDNA, RIKEN FULL-LENGTH ENRICHED LIBRARY,
CLONE:2310067K2O, FULL INSERT SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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PROSITE; PS00120; LIPASE_SER; 1.
SEQUENCE 395 AA; 44650 MW; 03F16D53373A4D57 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33.1%; Score 155; DB 11; 41.9%; Pred. No. 7.9e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AK010026; BAB26651.1; -.
MGD; MGI:1914967; 2310051B21Rik.
InterPro; IPR000073; Abhydrolase.
InterPro; IPR000379; Est_lip_thioest_actsite.
InterPro; IPR000734; Lipase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 31; Conservative
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196 ALAPVATVKYTESP 209
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Best Local Similarity
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us-09-699-652-12.rspt

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Query Match
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Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Atawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Atawa T., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Gadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Ruehl P., Lewis S., Matsuo Y., Nikaido I., Rochiwa H.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Brownstein M.J., Bult C., Redrim M., Hume D.A., Kamiya M., Lee N.H.,
RA Joros P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Gasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Winshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Winshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                              5
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                                                                                                                                                                                                                                                                                                                                                                                                                                   10 YWNWSWDDLVVNDLPAMVDFVVKQTGQ-KPHYVGHSMGTLVALAAFSEG-RVVSQLKSAA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
"Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                              2;
                                                                                                                                                                                                                                                                                                                         Query Match 33.1%; Score 155; DB 11; Length 395; Best Local Similarity 41.9%; Pred. No. 7.9e-10; Matches 31; Conservative 15; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
ADULT MALE TOWNE CDNA, RIKEN FULL-LENGTH ENRICHED LIBRARY,
CLONE:2310068C02, FULL INSERT SEQUENCE.
                                                                                                                                                                                Pfam; PF00561; abhyóroláse; 1.
PROSITE; PS00120; LIPASE_SER; 1.
SEQUENCE 395 AA; 44623 MW; 245055F5E7FF07C9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00561; abhydrolase; 1.
PROSITE; PS00120; LIPASE_SER; 1.
SEQUENCE 395 AA; 44638 MW; 4E52613BC98BAB3F CRC64;
                      Nature 409:685-690(2001).

EMBL; AK010093; BAB26697.1; -
MGD; MGI:1914967; 2310051B21Rik.

InterPro; IPR000073; Abhydrolase.

InterPro; IPR000739; Ext_lip_thioest_actsite.

InterPro; IPR000734; Lipase.
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InterPro; IPR000379; Est_lip_thioest_actsite.
InterPro; IPR000734; Lipase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             395 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [1]
SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-TONGUE;
MEDLINE-21085660; Pubmed-11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 409:685-690(2001).
EMBL; AK010103; BAB26703.1; -.
MGD; MGI:1914967; 2310051B21R1k.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          196 ALAPVATVKYTESP 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68 LLTPVAYLXHXNXP 81
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X RAWAI J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

X Rawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

A Arawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Ruchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Blake J., Boffelli D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Wanshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Nordoni A., Wang K., Wang K., Rawaji H., Kohtsuki S.,

Nordoni A., Wang K., Wang K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                       :| :|:|:: |||| :||:|:|| | |||||| || : ::|
136 FWARSFDEMAKYDLPATIDFIVQKTGQEKIHYVGHSQCTTIGFIAFSTNPALAKKIKRFY 195
                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                    10 YWNWSWDDLVVNDLPAMVDFVVKQTGQ-KPHYVGHSMGTLVALAAFSEG-RVVSQLKSAA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hayashizaki Y.; "Functional annotation of a full-length mouse cDNA collection.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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Length 395;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DCC-2001 (TrEMBLrel. 19, Last annotation update)
ADULT MALE TONGUE CDNA, RIKEN FULL-LENGTH ENRICHED LIBRARY,
CLONE: 2310076L13, FULL INSERT SEQUENCE.
                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00561; abhydrolase; 1.
PROSITE; PS00120; LIPASE_SER; 1.
SEQUENCE 395 AA; 44671 MW; E8936162510AA55C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33.1%; Score 155; DB 11;
41.9%; Pred. No. 7.9e-10;
live 15; Mismatches 26;
33.1%; Score 155; DB 11; 41.9%; Pred. No. 7.9e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mach: AK010203; BAB26766.1; -...
MGD; MGI:1914967; 2310051B21Rik.
InterPro; IPR0000073; Abhydrolase.
InterPro; IPR000379; Est_lip_thioest_actsite.
InterPro; IPR000734; Lipase.
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                                                                  15; Mismatches
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Matches 31; Conservative
                                                                     31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                               | ||| : : |
196 ALAPVATVKYTESP 209
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196 ALAPVATVKYTESP 209
                                                                                                                                                                                                                                                                        68 LLTPVAYLXHXNXP 81
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                                  Best Local Similarity
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Search completed: October 10, 2002, 02:13:37 Job time: 220 sec

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haemophilus

saccharomyc escherichia schizosach rattus norv bacillus th bacillus th bacillus st arabidopsis mus musculu escherichia escherichia escherichia

P07246 8 P37675 6 O13716 8 P013716 8 P018717 9 P51427 9 P51437 9

ADH3_YEAST YIAN_ECOLI YDZ9_SCHPO LIP1_RAT DNAK_BACTR DNAK_BACST RS5_ARATH CRAM_MOUSE YGBO_ECOLI DNAK_ESOLI

275 375 375 375 4424 402 606 607 607 1173 349 398 590

1152.7 122.7

ALIGNMENTS

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Search time 12.42 Seconds (without alignments) 280.576 Million cell updates/sec
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468
1 SSCTLRFQLYWNWSWDDLVV......PVAYLXHXNXPNXNPGWFXR
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	dros	m	canis	P04634 rattus norv	Q29458 bos taurus	P38571 homo sapien	Q920m5 mus musculu	Q64194 rattus norv			P27747 alcaligenes		Q9z268 mus musculu	P46782 homo sapien		066392 a poly-beta						Q9kgu6 pseudomonas			Q00554 oryctolagus			25234	916	17820]	_	92bn8 listeria	065731 cicer ariet
ID	LIP3_DROME	LIPG HUMAN	LIPG_CANFA	LIPG_RAT	LIPG_BOVIN	LICH_HUMAN	LICH_MOUSE	LICH_RAT	LIP1_DROME	DNAK_BACME	ACOC_ALCEU	TGL1_YEAST	RSG4_MOUSE	RS5_HUMAN	MPT5_MYCLE	PHBC_AZOCA	RSG4_HUMAN	RS5_MOUSE	RS5_RAT	RS5_DROME	RFAI_SALTY	DXR_PSEAE	TYPA_HAEIN	DXR_HELPJ	CFTR_RABIT	YBFF_ECOLI	ESL2_MYCPN	MDLA_PENCA	LYS2_SCHPO	DNAK_BACSU	DNAK_LISMO	ᆡ	RS5_CICAR
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7
Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; Science 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         126 WQIFWNFSWNEIGMYDVPAMIDYVLAKTGQQQQVQYVGHSQGTTVYLVWVSERPEYNDKIK 185
                                                                                                                                                                                                                                                                 -i- TISSUE SPECIFICITY: FAT BODY.
-i- DEVELOPMENTAL STAGE: ONLY AT LARVAL STAGES.
-i- SIMILARIY: PARTIAL WITH OTHER LIPASES (PANCREATIC, GASTRIC, HEPATIC, LINGUAL, LIPOPROTEIN, BACTERIAL, ETC.): ALSO SIMILAR TO LEPIDOPTERAN EGG-SPECIFIC AND YOLK PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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MEDLINE-8729724; PubMed-3304425;
BOGMER M.W., Angal S., Yarranton G.T., Harris T.J.R., Lyons A.,
King D.J., Pieroni G., Riviere C., Verger R., Lowe P.A.;
"Molecular cloning of a human gastric lipase and expression of the enzyme in yeast.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          194 LIPASE 3.

164 CHARGE RELAY SYSTEM (BY SIMILARITY).

369 CHARGE RELAY SYSTEM (BY SIMILARITY).

131 N-LINKED (GLCNAC. . .) (POTENTIAL).

44901 MW. A718D1D743673802 CRC64;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-APR-1988 (Rel. 07, Created)
01-APR-1988 (Rel. 07, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Triacylglycerol lipase, gastric precursor (EC 3.1.1.3) (Gastric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36.8%; Score 172; DB 1; Length 394; 44.2%; Pred. No. 2.5e-12; Live 18; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00561; abhydrolase; 1.
PROSITE; PS00120; LipasE_SER; 1.
Hydrolase; Lipid degradation; Signal; Glycoprotein.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AE003699; AAF54935.1; -.
FlyBase; FBgn0023495; Lip3.
InterPro; IPR000073; Abhydrolase.
InterPro; IPR000779; Est_lip_thioest_actsite.
InterPro; IPR000734; Lipase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; Y14367; CAA74737.1; -.
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Matches 34; Conservat
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164 1
369 3
131 1
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P07098;
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ACT_SITE
CARBOHYD
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LIPG_HUMAN
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                                                                                "Human gastric lipase. The N-terminal tetrapeptide is essential for lipid binding and lipase activity.";

Eur. J. Blochem. 182:495-499(1989).

-!- CATALYTIC ACTIVITY: Triacylglycerol + H(2)O - diacylglycerol + & fatty acid anion.

-!- SIMILARITY: PARTIAL WITH OTHER LIPASES (PANCEFATIC, GASTRIC, HEPATIC, LINGUAL, LIPOPROTEIN, BACTERIAL, ETC.).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRIACYLGLYCEROL LIPASE, GASTRIC.
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
N-LINKED (GLCNAC. . .) (POTENTIAL).
T -> A (IN DESNIP 814628).
/FITG-VAR. 011947.

W. CD3EE1621C014F0F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; A12714; CAA01053.1; -.
PIR; S04942; S04942.
PIR; S07145; S07145.
MIM; 601980; -.
InterPro; IPR000073; Abhydrolase.
InterPro; IPR000739; Est_lip_thioest_actsite.
InterPro; IPR000734; Lipase.
Pfam; PF00561; abhydrolase; I.
PROSITE; PS00120; LIPASE_SER; I.
Hydrolase; Lipid degradation; Glycoprotein; Signal; Polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LIPG_CANFA STANDARD; PRT; 398 AA.
P80035; 002857;
001-NOV-1991 (Rel. 20, Created)
15-JUL-1998 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Triacylglycerol lipase, gastric precursor (EC 3.1.1.3) (Gastric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33.3%; Score 156; DB 1; Length 398; 47.0%; Pred. No. 1.7e-10; ive 13; Mismatches 20; Indels
Biochim. Biophys. Acta 909:237-244(1987).
                                                                                                                                                                                                                                                                                                                                                             EMBL; X05997; CAA29413.1; -.
EMBL; X05997; CAA29414.1; ALT_INIT.
EMBL; A01046; CAA00125.1; -.
EMBL; A12714; CAA01053.1; -.
                                                    MEDLINE-89325292; PubMed-2753032; Bernbaeck S., Blaeckberg L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MM.
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Best Local Similarity 47.0%
Matches 31; Conservative
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197 ALAPVA 202
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NCBI_TaxID=10116;
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Q29458;
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CARBOHYD
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LIPG_BOVIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                   -1- CATALYTIC ACTIVITY: Triacylglycerol + H(2)0 = diacylglycerol + a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Gaps
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N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                  fatty acid anion.
SIMILARITY: PARTIAL WITH OTHER LIPASES (PANCREATIC, GASTRIC, HEPATIC, LINGUAL, LIPOPROTEIN, BACTERIAL, ETC.).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Triacylglycerol lipase, lingual precursor (EC 3.1.1.3) (Lingual
                                                                                                                                                                                       MEDLINE-92037652; PubMed-1935982;
Carritaer F., Moreau H.; Raphel V., Laugier R., Benicourt C.,
Junien J.-L., Verger R.;
"Purification and blochemical characterization of dog gastric
                                                                      Vaganay S., Joliff G., Bertaux O., Toselli E., Devignes M.D.,
Benicourt C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19; Indels
                                                                                                                         Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -> T (IN REF. 2).
E04D62F7518E386C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRIACYLGLYCEROL LIPASE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; S19539; S19539.
InterPro; IPR000073; Abhydrolase.
InterPro; IPR000073; Est_lip_thioest_actsite.
InterPro; IPR00073, Lipase.
Pfam; PF60561; abhydrolase; 1.
PROSITE; PS00120; LIPASE_SER; 1.
Hydrolase; Lipid,degradatlon; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32.9%; Score 154; DB 1;
45.5%; Pred. No. 2.9e-10;
tive 15; Mismatches 19
                                                                                                                                                                                                                                                                                                 Eur. J. Biochem. 202:75-83(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 32.9%
Best Local Similarity 45.5%
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              398 AA;
                                                                                                                                                                        SEQUENCE OF 20-59.
                                       SEQUENCE FROM N.A.
NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | ||||
197 ALAPVA 202
                                                           TISSUE-Stomach;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68 LLTPVA 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACT_SITE
ACT_SITE
CARBOHYD
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P04634;
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;
                                                                                                                                                                                                                                                                       fatty acid anion.
-!- MISCELLANEOUS: LINGUAL LIPASE IS SECRETED BY THE SEROUS (VON EBNER'S) GLANDS AT THE BACK OF THE RAT TONGUE.
-!- SIMILATIY: PRETIAL WITH OTHER LIPASES (PANCREATIC, GASTRIC, HEPATIC, LINGUAL, LIPOPROTEIN, BACTERIAL, ETC.).
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136 FWAFSFDEMAKYDLPATINFIVQKTGQEKIHYVGHSQGTTIGFIAFSTNPTLAKKIKTFY 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3.1.1.3) (Pregastric
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoldea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHARGE RELAY SYSTEM (BY SIMILARITY). CHARGE RELAY SYSTEM (BY SIMILARITY).
SEQUENCE FROM N.A.
MEDLINE=85215587; PubMed=3839077;
Docherty A.J.P., Bodmer M.W., Angal S., Verger R., Riviere C.,
Lowe P.A., Lyons A., Emtage J.S., Harris T.J.R.;
"Molecular cloning and nucleotide sequence of rat lingual lipase cDNA.";
                                                                                                                                                                                                                                    -!- CATALYTIC ACTIVITY: Triacylglycerol + H(2)0 - diacylglycerol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL)
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N-LINKED (GLCNAC. . ) (POTENTIAL)
N-LINKED (GLCNAC. . ) (POTENTIAL)
N-LINKED (GLCNAC. . ) (POTENTIAL)
E601854A92352EA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32.5%; Score 152; DB 1; Length 395; 40.5%; Pred. No. 4.9e-10; tive 17; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X02309; CAA26179.1; -.

EMBL; A01157; CAA00136.1; -.

PITS; A23045; LIRTT.

InterPro; IPR000073; Abhydrolase.

InterPro; IPR000073; Lipase.

InterPro; IPR000073; Lipase.

PFOM: PF00561; abhydrolase; 1.

PROSITE; PS00120; LIPASE_SER; 1.

Hydrolase; Lipid degradation; Glycoprotein; Signal.
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30-MAY-2000 (Rel. 39, Last annotation update)
Triacylglycerol lipase, pregastric precursor (EC
lipase) (GL) (Pregastric esterase) (GE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           397 AA.
                                                                                                                                                                                                               Nucleic Acids Res. 13:1891-1903(1985)
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30-MAY-2000 (Rel. 39, Last seq
30-MAY-2000 (Rel. 39, Last anno
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Matches 30; Conserv
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EMBL;
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136 FWAFSFDEMAEYDLPSTIDFILRRTGQKKLHYVGHSQGTTIGFIAFSTSPTLAEKIKVFY 195
SEQUENCE FROM N.A.
TISSUB-Tongue serous gland;
MEDIANE-95011625; PubMed=1926811;
Timmermans M.Y.J. Kupers L.P., Teuchy H.:
"The cDNA Sequence encoding bovine pregastric esterase.";
Gene 147:259-262(1994).
-:- CAPALYTIC ACTIVITY: Triacylglycerol + H(2)0 = diacylglycerol + a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 YWNWSWDDLVVNDLPAMVDFVVKQTGQKP-HYVGHSMGTLVALAAFSEGRVVSQ-LKSAA 67
                                                                                                                                                                                                                                                                                                                         TRIACYLGIYCEROL LIPASE, PREGASTRIC.
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND SEQUENCE OF 196-212; 277-297 AND 305-315.
MEDLINE-92042192; PubMed-1718995;
Anderson R.A., Sando G.N.;
                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: PARTIAL WITH OTHER LIPASES (PANCREATIC, GASTRIC, HEPATIC, LINGUAL, LIPOPROTEIN, BACTERIAL, ETC.).
                                                                                                                                                                                                                                                                                                                                                                                                                                                          5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Cloning and expression of cDNA encoding human lysosomal acid lipase/cholesteryl ester hydrolase. Similarities to gastric and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LICH_HUMAN STANDARD; PRT; 399 AA.
P38571; 016529; 056E010;
01-0CT-1994 (Rel. 30, Last sequence update)
01-0CT-1994 (Rel. 31, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Lysosomal acid Lipase/Cholesterryl ester hydrolase precursor (EC 3.1.1.13) (LAb.) (Acid cholesteryl ester hydrolase) (Sterol esterase) (Lipase A) (Cholesteryl esterase).
                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 397;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         20; Indels
                                                                                                                                                                                                                                                                                                                                                                                    N-LINKED (GLCNAC. . .) (Pr
F68977DED585EE36 CRC64;
                                                                                                                                                                                                                                        InterPro: IPR000073; Abhydrolase.
InterPro: IPR000379; Est_lip_thioest_actsite.
InterPro: IPR00734; Lipase.
InterPro: JR00561; abhydrolase; 1.
PR0STE: PS00120; LIPASE_SER; 1.
Hydrolase; Lipid degradation; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 145; DB 1;
Pred. No. 3.1e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         16; Mismatches
                                                                                                                                                                                                                                                                                                                 BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         lingual lipases.";
J. Biol. Chem. 266:22479-22484(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                31.0%;
                                                                                                                                                                                                                                                                                                                                                                                                45231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                    fatty acid anion.
                                                                                                                                                                                                                                                                                                                                                                                  326
397 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   196 ALAPVA 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68 LLTPVA 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                          28;
                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
CARBOHYD
SEQUENCE
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CARBOHYD
                                                                                                                                                                                                                                                                                                                                      ACT_SITE
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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-98295576; Pubmed-963819;
Ries S., Buechler C., Schindler G., Aslanidis C., Ameis D., Gasche C., Jung N., Schmitz G.;
Ries S., Buechler C., Schindler G., Aslanidis C., Ameis D., Gasche C., Jung N., Schmitz G.;
Figreen H., Schmitz G.;
Figreen H., Schmitz G.;
Figreen H., Schmitz G.;
Figreen Missense mutations in histidine-108 of lysosomal acid lipase cause cholesteryl ester storage disease in unrelated compound heterozygous and hemisygous individuals.";
Function: CRUCIAL FOR THE INTRACELLULAR HYDROLYSIS OF CHOLESTERYL ESTERS AND TRIGLYCERIDES THAT HAVE BEEN INTERNALIZED VIA RECEPTORMEDIATED ENDOCYTOSIS OF LIPOPROTEIN PARTICLES. IMPORTANT IN MEDIATED ENDOCYTOSIS OF LIPOPROTEIN UPTAKE ON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUPPRESSION OF HYDROXYMETHYLGLUTARYL-COA REDUCTASE AND ACTIVATION OF ENDOGENOUS CELLULAR CHOLESTERYL ESTER FORMATION.

CATALYTIC ACTIVITY: A steryl ester + H(2)0 = a sterol + a fatty
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Lysosomal.

DISEASE: DEFECTS IN LIPA ARE THE CAUSE OF THE SEVERE INFANTILE-ONSET WOLMAN DISEASE (WD) AND THE MILDER LATE-ONSET CHOLESTERYL STORAGE DISEASE (CESD).

SIMILARIY: PARTIAL WITH OTHER LIPASES (PANCREATIC, GASTRIC, HEPATIC, LINGUAL, LIPOPROTEIN, BACTERIAL, ETC.).
                                                                                                                                                                                                                                                                                                                    Du H., Witte D.P., Grabowski G.A.; "Issue and cellular specific expression of murine lysosomal acid lipase mRNA and protein."; "Lipid Res. 37:937-949(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anderson R.A., Byrum R.S., Coates P.M., Sando G.N.; "Mutations at the lysosomal acid cholesteryl ester hydrolase gene
                                       Greten H.; molecular cloning of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 91:2718-2722(1994)
                                       Ameis D., Merkel M., Eckerskorn C., "Purification, characterization and
                                                                                                        hepatic lysosomal acid lipase.";
Eur. J. Biochem. 219:905-914(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VARIANTS CESD ARG-129 AND PRO-129.
                                                                                                                                                                                                                                                                                    MEDLINE=96363957; PubMed=8725147;
MEDLINE=94155897; PubMed=8112342;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-94195814; Pubmed-8146180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB60327.1; JOINED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOINED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOINED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOINED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M74775; AAA59519.1; -. EMBL; U04285; AAB60327.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAA83495.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BC012287; AAH12287.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB60327.1;
AAB60327.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB60327.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB60327.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               locus in Wolman disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VARIANT CESD/WD PRO-200
                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             U04293; N
X76488; C
Z31690; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            004291;
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EMBL;
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HYDROLASE
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33.8%;
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                                                                                                                                                                                                                                                                                                                                                                                          45551
                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :| || | : |
197 VLAPVLSLNFASGP 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68 LLTPVAYLXHXNXP
                                                                                                                                                                                                                                                                                                                                                                               319
397 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                             Best_Local Similarity
Matches 25; Conserv
                                                                                                                                                                                                                                                                                      Hydrolase;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LICH_RAT
Q64194;
                                                                                                                                                                                                                                                                                                                                   ACT_SITE
CARBOHYD
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CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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qq
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"Tissue and cellular specific expression of murine lysosomal acid
lipase mRNA and protein."; 2949(1996).
J. Lipid Res. 37.937-949(1996).
-!- FUNCTION: CRUCIAL FOR THE INTRACELLULAR HYDROLYSIS OF CHOLESTERYL
ESTERS AND TRIGLYCERIDES THAT HAVE BEEN INTERNALIZED VIA RECEPTOR-
MEDIATED ENDOCYTOSIS OF LIPOPROTEIN PARTICLES. IMPORTANT IN
MEDIATING THE EFFECT OF LDL (LOW DENSITY LIPOPROTEIN) UPTAKE ON
                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                           LYSOSOMAL ACID LIPASE/CHOLESTERYL ESTER
                                                                                                                                                                                                                                                                                                                                                      10 YWNWSWDDLVVNDLPAMVDFVVKQTGQKP-HYVGHSMGTLVALAAFSE-GRVVSQLKSAA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata, Craniata; Vertebrata, Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                              SIMILARITY). SIMILARITY).
                                                                                                                               . .) (POTENTIAL).
                                                                                                                                          (POTENTIAL).
                                                                                                                                                (POTENTIAL)...) (POTENTIAL)...
                                                                                                                                                                     .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                   'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Lysosomal acid ilpase/cholesteryl ester hydrolase precursor
(EC 3.1.1.13) (LAL) (Acid cholesteryl ester hydrolase) (Sterol
              InterPro; IPR000073; Abhydrolase.
InterPro; IPR000379; Est_lip_thioest_actsite.
InterPro; IPR000734; Lipase.
Pfam: PF00561; abhydrolase; 1.
PROSITE; PS00120; LIPASE_SER; 1.
Hydrolase; Lipid degradation; Glycoprotein; Signal; Lysosome;
                                                                                                                                                                                                                                                                                                                 Length 399;
                                                                                                                                                                                                                                                                                                                                  31; Indels
                                                                                                                                                                                                                                                                                    55F27391306B609A CRC64;
                                                                                                                              N-LINKED (GLCNAC. .) (
P -> T.
                                                                                                                                                                                                                                      /FTId=VAR_004249. L \rightarrow P \text{ (IN CESD AND WD)}
                                                                                                              CHARGE RELAY SYSTEM
CHARGE RELAY SYSTEM
                                                                                                                                                                                                                                                        TIG=VAR_004250.
-> R (IN REF. 3).
-> L (IN REF. 4).
                                                                                                                                                                                                                                                                                                               29.1%; Score 136; DB 1; 35.4%; Pred. No. 3.4e-08; iive 18; Mismatches 31
                                                                                                                                                                                                                   TIG=VAR_004248
                                                                                                                                                                                                 /FTIG-VAR_004247
                                                                                                                                                                                                            -> P (IN CESD)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          397 AA
                                                                                  POTENTIAL
                                                                                                                                                                                                                    FTIG=VAR
                                                                                                      HYDROLASE
                                                                                                                                                                                                                                                          /FTIG=VAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-C5781/6 X CBA; TISSUE-Liver;
MEDLINE-96363957; Pubmed-8725447;
                                                                         Disease mutation; Polymorphism.
                                                                                                                                                                                                                                                                                     MW.
                                                                                                                                                                                                                                                                                                                                                                                                            199 ALGPVASVAFCTSPMAKLG 217
                                                                                                                                                                                                                                                                                                                                                                                          68 LLTPVAYLXHXNXPNXNPG 86
                                                                                                                                                                                                                                                                                    45415
                                                                                                                                                                                                                                                                                                                        Local Similaricy ... hes 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                 101
161
273
321
16
                                                                                                                                                                                                           129
                                                                                                                                                                                                                              129
                                                                                                                                                                                                                                                                   23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LIPA OR LIP1.
Mus musculus (Mouse).
A39315; A39315.
                                                                                                                                                                                                                                                                  23
29
399 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
                                                                                                                                                                                                                                                200
                                                                                                              174
374
36
72
101
161
161
273
321
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                                                                                                                                                                                                                             129
        278000;
                                                                                                                                                                                                                                                                                                                                                                                                                                               LICH_MOUSE
ID LICH_MOUSE
AC Q920M5;
                                                                                                                                                                     CARBOHYD
CARBOHYD
                                                                                                                       ACT_SITE
CARBOHYD
                                                                                                              ACT_SITE
                                                                                                                                          CARBOHYD
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                                                                                                                                                                                                                                                                   CONFLICT
                                                                                                                                                                                                                                                                           CONFLICT
                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                         VARIANT
                                                                                                                                                                                                           VARIANT
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                                                                                  SIGNAL
                                                                                           CHAIN
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Matches
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                                                                                                                                                                                                                         most tissues. High
SUPPRESSION OF HYDROXYMETHYLGLUTARYL-COA REDUCTASE AND ACTIVATION OF ENDOGENOUS CELLULAR CHOLESTERYL ESTER FORMATION (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :| :|:|:: |||| ::::::|||: :|||| : ||||: :::|
137 FWAFSFDEMAKYDLPASINYILNKTGQEQIYYVGHSQCCTIGFIAFSQMPELAKKIKMFL 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Rat).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                              SUBCELLULAR LOCATION: Lysosomal.

TISSUE SPECIFICITY: Expressed at low levels in most tissues. Hig level expression is found in hepatocytes and splenic and thymic cells. Very high level expression is observed in cells of the small intestinal villi, the zona fasciculata and reticularis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LYSOSOMAL ACID LIPASE/CHOLESTERYL ESTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 YWNWSWDDLVVNDLPAMVDFVVKQTGQKP-HYVGHSMGTLVALAAFSE-GRVVSQLKSAA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
N-LINKED (GLCNAC. . ) (POTENTIAL).
                                                                     similarity).
CATALYTIC ACTIVITY: A steryl ester + H(2)0 = a sterol + a fatty
                                                                                                                                                                                                                                                                                                                                                                                                           epithelium.
SIMILARITY: PARTIAL WITH OTHER LIPASES (PANCREATIC, GASTRIC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
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01-MAR-2002 (Rel. 41, Last sequence update)
Lysosomal acid lipase/cholesterryl ester hydrolase precursor (EC 3.1.1.13) (LAL) (Acid cholesteryl ester hydrolase) (Sterol esterase) (Lipase A) (Cholesteryl esterase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glycoprotein; Signal; Lysosome.
                                                                                                                                                                                                                                                                                                                                                                            the adrenal cortex, pancreatic acini, and renal tubular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 397;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-LINKED (GLCNAC. ..) (P. F886C39E1CCFA91F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HEPATIC, LINGUAL, LIPOPROTEIN, BACTERIAL, ETC.).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 129; DB 1;
Pred. No. 2.1e-07;
); Mismatches 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MICHARD MILEGE 196789; Lipl.
InterPro; IPR000073; Abhydrolase.
InterPro; IPR000734; Lipase.
InterPro; IPR000734; Lipase.
InterPro; IPR000734; Lipase; IPR00178; PR00120; LIPASE_SER; IPR0517E; PS00120; LIPASE_SER; IPR0517E; Lipid degradation; Glycoprotein; S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          397 AA.
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Ephydroidea;

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;
                               Nakagawa H., Matsubara S., Kuriyama M., Yoshidome H., Fujiyama J.,
Yoshida H., Osame M.;
"Cloning of rat lysosomal acid lipase cDNA and identification of the
mutation in the rat model of Wolman's disease.";
J. Lipid Res. 36.2212-2218(1995).

-! FUNCTION: CRUCIAL FOR THE INTRACELLULAR HYDROLYSIS OF CHOLESTERYL
ESTERS AND TRIGLYCERIDES THAT HAVE BEEN INTERNALIZED VIA RECEPTOR-
MEDIATING THE EFFECT OF LIPOPROTEIN PARTICLES, IMPORTANT IN
SUPPRESSION OF HYDROXYMETHYLGLUTARYL-COA REDUCTASE ON
SUPPRESSION OF HYDROXYMETHYLGLUTARYL-COA REDUCTASE AND ACTIVATION
OF ENDOGENOUS CELLULAR CHOLESTERYL ESTER FORMATION (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LYSOSOMAL ACID LIPASE/CHOLESTERYL ESTER HYDROLASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10 YWNWSWDDLVVNDLPAMVDFVVKQTGQKPHY-VGHSMGTLVALAAFSE-GRVVSQLKSAA 67
                                                                                                                                                                               CATALYTIC ACTIVITY: A steryl ester + H(2)0 = a sterol + a fatty
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY).
SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL)
                                                                                                                                                                                                                 PARTIAL WITH OTHER LIPASES (PANCREATIC, GASTRIC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GLCNAC...) (PULDAL...)
(GLCNAC...) (POTENTIAL)
(GLCNAC...) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                            Glycoprotein; Signal; Lysosome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26.5%; Score 124; DB 1; Length 397; 35.1%; Pred. No. 8.1e-07; ive 17; Mismatches' 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97A38595A0523947 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHARGE RELAY SYSTEM (BY
CHARGE RELAY SYSTEM (BY
N-LINKED (GLCNAC. . .) (
                                                                                                                                                                                                                  SIMILARITY: PARTIAL WITH OTHER LIPASES (PANCREAT:
HEPATIC, LINGUAL, LIPOPROTEIN, BACTERIAL, ETC.).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       •
                                                                                                                                                                                                                                                                                                                               EMBL; S81497; AAB36043.2; -.
EMBL; S81497; AAB36043.2; -.
InterPro; IPR000073; Abhydrolase.
TrierPro; IPR000379; Est_lip_thioest_actsite.
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01-MAR-2002 (Rel. 41, Last annotation update)
Lipase 1 precursor (EC 3.1.1.-).
LIPI OR CG7279.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             439 AA.
                                                                                                                                                                                                                                                                                                                                                                                  Pfan, PF00561; abhydrolase; 1.
PROSITE; PS00120; LIPASE_SER; FALSE_NEG.
Hydrolase; Lipid degradation; Glycoprote
                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-LINKED
                                                                                                                                                                                                      SUBCELLULAR LOCATION: Lysosomal.
                      MEDLINE-96129534; PubMed-8576647;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LIPILDROME STANDARU;
046107; 09VRR6;
16-OCT-2001 (Rel. 40, Created)
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99
159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               319
397 AA;
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Best Local Similarity
FROM N.A.
                                                                                                                                                                    similarity)
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CARBOHYD
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CARBOHYD
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Galle R.F., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., Gocayge R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Worthan J.R., Yandell M.D., Zhang Q., Chen L.X., RA Aradon R.C., Rogers Y.-H.C., Blazej R.G., Change M., Miklos G.L.G., Mandon R.C., Batter E.G., Helt G., Nolson C.R., Miklos G.L.G., Abril J.F., Agbayani A., An H.-J., Andrews-Ffannkoch C., Baldwin D., Ballew R.M., Basu A., Baxendal J., Bayetakaragul L., Beasley E.M., Ballew R.M., Basu A., Baxendal J., Bayetakaragul L., Beasley E.M., Burtis N.C., Busam D.A., Butler H., Caddeu E., Center A., Chadra I., Abrit J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Andrews D., Burtis N.C., Busam D.A., Dahlke C., Davenport L.B., Davies P., Andrews M., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Bodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., RA Burtis N.L., Evangelista C.C., Ferraz C., Ferriar S., Pleischman W., Rallen R., Gorrell J.H., Gu Z., Genbart W.M., Glasser K., Gong F., Gorrell J.H., Gu Z., Genbart W.M., Glasser K., Julian R., Mouston K.A., Howland T.J., Wei M.-H., Ibegwan C., Julian B.E., Rodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lasko P., Lei Y., Levitsky A.A., Li J., Ul Z., Liang Y., Lia Z., Lasko P., Lei Y., Levitsky R.A., Li J., Ul J., Li Z., Liang Y., Lia Z., Month S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Merkulov G., Milshina N.V., Mobarty C., Morberson D., Merkulov G., Milshina N.V., Mobarty C., Morberson D., Merkulov G., Milshina N.V., Nobarty C., Wolley R., Sun E., Santh H., Shienet K., Wassarman D.A., Nixon K., Nusskern D.Y., Purt, V., Wang X., Yel J., Yeh R.-F., Zaveri J.S., Zhan M., Stung R., Sante R., Wang Z.-Y., Wassarman D.A., Walley C., Shang G., R., Wang Z.-Y., Wassarman D.A., Wolferson M., Stung G., Zhao O., Zhao C., Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    European Bioinformatics Institute. There are no restrictions on by non-profit institutions as long as its content is in no
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-:- SIMILARITY: PARTIAL WITH OTHER LIPASES (PANCREATIC, GASTRIC, HEPATIC, LINGUAL, LIPOPROTEIN, BACTERIAL, ETC.). ALSO SIMILAR TO LEPIDOPTERAN EGG-SPECIFIC AND YOLK PROTEINS.
                                                                                                                                                                                                                   MEDLINE-98227315; PubMed-9566193;
Pistillo D., Manzi A., Tino A., Pilo Boyl P., Graziani F., Malva The Drosophila melanogaster lipase homologs: a gene family with tissue and developmental specific expression.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000073; Abhydrolase.
InterPro; IPR000379; Est_lip_thioest_actsite.
InterPro; IPR000734; Lipase.
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Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-BERKELEY;
MEDLINE-20196006; PubMed-10731132;
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                                                                                                                                      SEQUENCE OF 7-433 FROM N.A.
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                                      BI_TaxID=7227;
                                                                                                                                                                                      STRAIN-CANTON-S;
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BY SIMILARITY. 29DF856DC5FAEC14 CRC64;

65119 MW;

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604 AA;
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                                                                                                                                                             ACOC_ALCEU
                                                                                                                                                                                                                                                                                Ralstonia.
 INIT_MET SEQUENCE
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BINDING
                                         Query Match
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                                                                                                                                       RESULT 11
ACOC_ALCEU
                                                              Matches
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                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                               3;
                                                                                                                                                                                                                                                 162 FWDFSWHEIGMYDLPAMIDHVLKVTGFPKLHYAGHSQCCTSFFVMCSMRPAYNDKVVSM- 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE—87331083; PubMed=3035506;
Sussman M.D., Setlow P.;
"Nuclectide sequence of a Bacillus megaterium gene homologous to the dnaK gene of Escherichia coli.";
Nucleic Acids Res. 15:3923-3923(1987).
-! FUNCTION: ACTS AS A CHARERONE (BY SIMILARITY).
-! INDUCTION: BY STRESS CONDITIONS E.G. HEAT SHOCK (BY SIMILARITY).
-! SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
                                           N-LINKED (GLCNAC. ) (POTENTIAL).
T -> I (IN REF. 1).
Y -> F (IN REF. 1).
O -> E (IN REF. 1).
                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                    10 YWNWSWDDLVVNDLPAMVDFVVKQTG-QKPHYVGHSMG-----TLVALAAFSEGRVVSQL 63
                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1988 (Rel. 09, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Chaperone protein dnaK (Heat shock protein 70) (Heat shock 70 kDa protein) (HSP70).
                                                                                                                                                                                                               10;
                                                                                                                                                                                           Length 439;
                                                                                                                                                                                                              23; Indels
                                                                                                                                                           9E32E20BEAE93E3F CRC64;
           Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
NCBL_TaxID=1404;
                                                                                                                                                                                          24.6%; Score 115; DB 1; 36.6%; Pred. No. 9.8e-06; iive 12; Mismatches 23
                                                                                                                                                                                                                                                                                                                                                         604 AA.
          Signal; Gl
POTENTIAL.
                                LIPASE 1.
                                         POLY-GLU
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PRINTS; PR00301; HEATSHOCK70.
PROSITE; PS00329; HSP70_1; 1.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
Chaperone; ATP-binding; Heat shock.
                                                                                                                                                                                                                                                                                                                                                          PRT;
PROSITE; PS00120; LIPASE SER;
                                                                                                                                                             ¥.
           Lipid degradation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; Y00154; CAA68348.1; -
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                                                                                                                                                             50660
                                                                                                                                                                                                   Local Similarity 36.6 nes 26; Conservative
                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                               439
197
197
124
151
346
426
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                                                                                                                                                                                                                                                                                                    221 --- QALAPAVY 228
                                                                                                                                                                                                                                                                               64 KSAALLTPVAY 74
                                                                                                                                                  412
439 AA;
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30
197
393
393
151
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P05646;
            Hydrolase;
                                        DOMAIN
ACT_SITE
ACT_SITE
CARBOHYD
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DNAK_BACME
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                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACETOIN CATABOLISM.
-!- CATALYTIC ACTIVITY: Acetyl-CoA + dihydrolipoamide = CoA + S-
excetylalidydrolipoamide.
-!- COFACTOR: THE E2 COMPONENT CONTAINS ONE COVALENTLY-BOUND LIPOYL
COFACTOR (PROBABLE).
-!- PATHWAY: ACETOIN CATABOLISM.
-!- INDUCTION: BY GROWTH ON ACETOIN.
-!- SIMILARITY: CONTAINS 1 LIPOYL-BINDING DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                            01-MG-1992 (Rel. 23, Created)
01-DE-1992 (Rel. 24, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Dihydrolipoamide acetyltransferase component of acetoin cleaving system (EC 2.3.1.12) (Acetoin dehydrogenase E2 component)
(Fast-migrating protein) (FMP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 eutrophus H16 aco operon genes involved in acetoin catabolism."; J. Bacteriol. 173:4056-4071(1991).
                                                                                                                                                                                      ,
,
                                                                                                                                                 23 LPAMVDFVVKQTGQKPHYVGHSMGTLVALAAFSEGRVVS-QLKSAALL--TPVA 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alcaligenes eutrophus (Ralstonia eutropha).
Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
                                  Length 604;
                                                                                         17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LIPOYL (BY SIMILARITY).
9D5CE1F83E94892F CRC64;
                              Score 73; DB 1;
Pred. No. 0.93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Interpro; IPR003089; AB_hydrolase.
InterPro; IPR000073; Abhydrolase.
InterPro; IPR000089; Blotin_lipoyl.
InterPro; IPR000379; Est_lip_thioest_actsite.
InterPro; IPR003016; Lipoyl.
15.6%; SCOL.

9 38.9%; Pred. No. U....

12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                373 AA
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                                                                                                                                                                                                                                                                                                                                                                PRT;
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                                                                                         21; Conservative
                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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                                                             Best Local Similarity
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Length 373;

DB 1;

15.3%; Score 71.5;

799 AA

PRT;

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16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                       RasGAP-activating-like protein 1. RASAL1 OR RASAL.
          STANDARD;
                                                                                                                                                                                                                                     Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
      RSG4_MOUSE
Q9Z268;
             HIDDELLAR SETTEMENT OF THE PRESENCE OF THE PRESENCE OF THE PRESENCE OF THE PROPERTY OF THE PRO
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                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE-92245761; PubMed=1574929; Abraham P.R., Mulder A., Van'T Riet J., Planta R.J., Raue H.A.; Molecular cloning and physical analysis of an 8.2 kb segment of chromosome XI of Saccharomyces cerevisiae reveals five tightly linked
                                                                                                                                               Rad M.R., Xu G., Kirchrath L., Fritz C., Keuchel H., Hollenberg C.P., Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                      11 WNWSWDDL-----VVNDLPA------WDF-VK---QTG-QKPHYVGHSM 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 YWNWSWDDLVVNDLPAMVDFVVKQTG-QKPHYVGHSMGTLVALAAFSEGRVVSQLKS--- 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
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                                     20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Triglyceride lipase-cholesterol esterase (EC 3.1.1.-). TGL1 OR YKL140W OR YKL5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62979 MW; 32D1F230701CB083 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SGD; S0001623; TGL1.
InterPro: IPR000073; Abhydrolase.
InterPro: IPR000079; Est_lip_thioest_actsite.
Pro: PF00561; abhydrolase; 1.
Hydrolase; Lipid degradation.
SEQUENCE 548 AA; 62979 WW; 32D1F230701CBC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    548 AA.
      0.8;
                                         Mismatches
                                                                                                                                                                                                                                                                           210 GGGVAAQLAVDAPQRVL----SVALVSPVGF 236
                                                                                                                                                                                                                                  46 GTLVA - - LAAFSEGRVVSQLKSAALLTPVAY 74
          Pred. No.
                                     10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Rel. 28, Created)
(Rel. 28, Last sequence)
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33.0%;
                                         30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (east 8:227-238(1992).
      Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         226 AIAPAMTP 233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1994
01-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGL1_YEAST
P34163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            genes.
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                                         Matches
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RSG4_MOUSE

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                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-98426153; PubMed=9751798;
Allen M., Chu S., Brill S., Stotler C., Buckler A.;
Allen M., Chu S., Brill S., Stotler C., Buckler A.;
Restricted tissue expression pattern of a novel human rasGAP-related gene and its murine ortholog.";
Gene 218:17-25(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 LRFQLYWNWSWDDLVVNDLPAMVDFVVKQTGQKP-------HYVGHSMGTLVAL 51
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                 -!- FUNCTION: PROBABLE INHIBITORY REGULATOR OF THE RAS-CYCLIC AMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14.5%; Score 68; DB 1; Length 799; 30.4%; Pred. No. 4.8; tive 7; Mismatches 25; Indels
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E42F54B677F52269 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS50003; PH_DOMAIN; 1.
PROSITE; PS00499; C2_DOMAIN.1; 2.
PROSITE; PS50004; C2_DOMAIN.2; 2.
PROSITE; PS0500509; RAS_GTPASE_ACTIV.1; FALSE_NEG.PROSITE; PS50018; RAS_GTPASE_ACTIV_2; 1.
                                                                                                                                                                                                                                                                                                                                                                         -1- SIMILARITY: CONTAINS 2 C2 DOMAINS.
-1- SIMILARITY: CONTAINS 1 PH DOMAIN.
-1- SIMILARITY: CONTAINS 1 BTK DOMAIN.
-1- SIMILARITY: CONTAINS 1 RAS-GAP DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C2 DOMAIN 1.
C2 DOMAIN 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RAS-GAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF086714; AAD09007.1; -. HSSP; P04410; 1A25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGD; MGI: 1330842; Rasall.
InterPro; IPR001562; BTK.
InterPro; IPR001562; BTK.
InterPro; IPR0010008; C2.
InterPro; IPR001936; RasGAP.
Pfam; PF00779; BTK; 1.
Pfam; PF00169; PH; 1.
Pfam; PF00169; PH; 1.
Pfam; PF00169; PH; 1.
SMART; SM00107; BTK; 1.
SMART; SM00239; C2; 2.
SMART; SM00239; C2; 2.
SMART; SM00233; PH; 1.
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89428 MW;
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Best Local Similarity 30.4
Matches 21; Conservative
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MPT51 antigen precursor.
MPT51 OR ML0098.
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                                                                                                                                                                                                                                                                                                                                                                                  proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 QLYWNWSWDDLVVNDLPAMVDFVVKQTGQKPHYVGHSMGTLVALAAFSEGR---VVSQLKS 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S5,
                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: BELONGS TO THE S7P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                       Frigerio J.-M., Dagorn J.C., Iovanna J.L.; "Cloning, sequencing and expression of the L5, L21, L27a, L28, S9, S10 and S29 human ribosomal protein mRNAs."; Biochim. Biophys. Acta 1262:64-68(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14.4%; Score 67.5; DB 1; Length 204; 29.7%; Pred. No. 1.2; tive 15; Mismatches 25; Indels
                                                                                                                                                                                                                                                                           MEDLINE-98248690; PubMed-9582194;
Kenmochi N., Kawaguchi T., Rozen S., Davis E., Goodman N., Hudson T.J., Tanaka T., Page D.C.;
"A map of 75 human ribosomal protein genes.";
Genome Res. 8:509-523(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               204 AA; 22777 MW; E15FB763897FC748 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MATES_MYCLE STANDARD; PRT; 301 AA. 005868; 050207; 01-NOV-1995 (Rel. 32, Created) 16-CCT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                  01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
40S ribosomal protein S5.
                                                      204 AA
                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00177; Ribosomal_S7; 1.
ProDom; PD000817; Ribosomal_S7; 1.
PROSITE; PS00052; RIBOSOMAL_S7; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; P17291; 1RSS.
MIM; 603630; -.
InterPro; IPR000235; Ribosomal_S7.
                                                                                                                                                                                                              MEDLINE=95290496; PubMed=7772601;
                                                                          01-NOV-1995 (Rel. 32, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AB007149; BAA25815.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U14970; AAA85658.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 29.7
hes 19; Conservative
                                                      STANDARD;
                                                                                                                                   Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P17291; 1RSS.
                                                                                                                                                                                        SEQUENCE FROM N.A.
253 VRLTEDRVL 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ribosomal protein.
                                                                                                                                                                                                    TISSUE=Colon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66 AALL 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMMM 78
                                                     RS5_HUMAN
P46782;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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MPT5_MYCLE
                               RESULT 14
RS5_HUMAN
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S -> F (IN REF. 1).
APQLAAMSGDIVGAIR -> GAAVGCYVGRYRRHSLGRNQ
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                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=21128732; PubMed=11234002;
Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R.,
Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,
Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LLAGDPEWSRKCHVSATESSPGRLPCRWRPSWRWPLWLW
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                                                                Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rinke de Wit T.F., Bekelie S., Osland A., Wieles B., Janson A.A.M.,
Thole J.E.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Signal; Antigen; Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The Mycobacterium leprae antigen 85 complex gene family: identification of the genes for the 85A, 85C, and related MPT51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Infect. Immun. 61:3642-3647(1993).
-!- SUBCELLULAR LOCATION. Secreted.
-!- SIMILARITY: TO OTHER MYCOBACTETUM A85 ANTIGENS AND TO THE
N-TERMINAL OF C.GLUTAMICUM PS1 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 65; DB 1; Length 301; Pred. No. 3.5;
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                                                                                                                                                                                                                            Yin Y.;
"Studies of MPT51 like protein of Mycobacterium leprae.";
Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
Mycobacterium leprae.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3E686C805BFAB28 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Massive gene decay in the leprosy bacillus."; Nature 409:1007-1011(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; 221949; CAA79947.1; -.
Leproma; ML0098; -.
HSSP; P31953; 1DQZ.
InterPro; 1PR000801; Esterase_put.
Pfam; PF00756; Esterase; 1.
Transferase; Acyltransferase; Signal; SIGNAL
37 301 MPT51 AN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (IN REF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 1-220 FROM N.A. MEDLINE=93366419; Pubmed=8359887;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; D50488; BAA09079.1; -.
EMBL; AL583917; CAC29606.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          301 AA; 31191 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13.9%;
31.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                  NCBI_TaxID=1769;
                                                                                                                                                                                                 STRAIN-THAI53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Db
```

56 EGR 58 | 162 PDR 164 Oy Dp

Search completed: October 10, 2002, 02:14:31 Job time: 214 sec

```
GenCore version 4.5

Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 10, 2002, 02:10:32; Search time 14.1 Seconds

(without alignments)
613.336 Million cell updates/sec

Title: US-09-699-652-12

Perfect score: 468
Sequence: 1 SSCTLRFQLYWNWSWDDLVV.......PVAXLXHXNXPNNRGWPXR 90

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000
```

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: PIR_71:*
1: pir1:*
2: pir2:*
3: pir2:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	probable	triacylglycerol li	triacylglycerol li	hypothetical prote		hypothetical prote	-	hypothetical prote	acid	acid	Д	hypothetical prote		triglyceride lipas	triglyceride lipas	probable triacylgl	probable esterase/	unknown protein F2	probable membrane	F9L1.1 protein - A	hypothetical prote	conserved hypothet	hypothetical prote	hypothetical prote	arylesterase-relat	2-hydroxy-6-oxohep	hypothetical prote	probable triglycer	esterase, probable
SUMMARIES	OI.	S	S07145	LIRTT	T22290	н88930	T22675	JC4017	T33198	S41408	G01416	JT0949	T20480	G89074	T39540	T41053	T43170	F83425	G96764	S64842	D86284	C97494	AE2712	T31611	E75620	G87675	C64612	B71903	T39443	B90424
	DB	7	7	-	7	7	7	П	7	7	7	7	~	7	7	~	~	~	7	7	7	~	~	7	~	7	7	~	7	7
	Query Match Length	344	398	395	411	405	405	397	403	399	399	559	426	411	443	467	413	336	460	538	523	207	207	1585	369	438	241	241	460	353
ď	Query Match	36.3	33.3	32.5	ij.	31.1	31.1	31.0	29.8	29.1	29.1	26.9	26.3	26.1	25.3	21.6	20.4		13		18	18.2	18.2	17.0	•		16.0	•	15.9	15.6
	Score	170	156	152		マ	145.5	145	139.5	136	136	126	123	122	118.5	101	95.5	93.5	92.5	90.5	86.5	85	82	79.5	77	97	75	75	74.5	73
	Result No.	-	2	e	4	2	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	53

dnaK-type molecula	dihydrolipoamide S	probable triacylgl	probable hydrolase	probable membrane	ribosomal protein	40S ribosomal prot	MPT51 protein - My	probable esterase	hypothetical prote	antigen 85C, mycol	hypothetical prote	ribosomal protein	esterase/lipase 2	rfaI protein - Sal	probable ATSEH - A
139837	D42462	837969	F75443	S64754	S55916	F84790	S32111	T00809	T33322	B86921	T40678	R3RT5	A99516	S12097	D71425
7	-	7	7	7	7	7	7	7	7	7	~	Н	7	7	7
605	374	548	236	573	204	207	220	284	292	301	1097	204	290	133	193
15.6	15.3	14.7	14.5	14.5	14.4	14.4	13.9	13.9	13.9	13.9	13.8	13.7	13.7	13.6	13.6
73	71.5	69	89	68	67.5	67.5	65	65	65	. 65	64.5	64	64	63.5	63.5

ALIGNMENTS

	RESULT 1 R84526
-	probable lysosomal acid lipase [imported] - Arabidopsis thaliana (;Species: Arabidopsis thaliana (mouse-ear cress) (;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
	C;Accession: E84326 R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Bentto, M.I.; Town, C.D.; Fujil, C.Y M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
	Availe 40., fol. 700, 12.700, 12.700. Availe of chromosome 2 of the plant Arabidopsis thaliana. A.Reference number: A84420; MUID:20083487
	A; Accession: E04920 A; Status: preliminary A; Molecule type: DNA A; Residues: 1-344 <sto></sto>
	A;Cross-reterences: GB:AE002093; NID:g4585908; PIDN:AAD25509.1; GSPDB:GNU0139 C;Genetics: A;Gene: At2g15230 A;Map position: 2
	Query Match 36.3%; Score 170; DB 2; Length 344; Best Local Similarity 38.9%; Pred. No. 1.2e-11; Matches 28; Conservative 17; Mismatches 27; Indels 0; Gaps 0;
	Qy 10 YWNWSWDDLVYNDLPAMVDFVVKQTGQKPHYVCHSMGTLVALAAFSEGRVVSOLKSAALL 69
	Qy 70 TPVAYLXHXNXP 81 1:1
	RESULT 2 S07145
	triacylglycerol lipase (EC 3.1.1.3) precursor, gastric - human
	1
	R;Bodmer, M.W.; Angal, S.; Yarranton, G.T.; Harris, T.J.R.; Lyons, A.; King, D.J.; Pi Biochim. Biophys. Acta 909, 237-244, 1987
	A;Title: Molecular cloning of a numan gastric lipase and expression of the enzyme in A;Reference number: \$07145; MUID:87299724 A;Recession: \$07145
	A; Molecule type: mRNA A; Residues: 1-398 <bod1> A; Cross-references: EMBL:X05997; NID:g31771; PIDN:CAA29413.1; PID:g758063</bod1>
	A;Accession: S27102 A;Molecule type: protein A;Residues: 20-24,'X',26,'X',28-33,'X',35-42,'X',44,'X',46-48,'X',50,'X',52,'X',54-56

N

4;

Gaps

```
protein R1G11.14 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Old #sequence_revision 10-May-2001 #text_change 24-May-2001
C;Accession: H88930
R;Ancopymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating bio A;Reference number: A75000; MUID: 990605013; PMID: 9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; A;Status: preliminary
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; A;Molecule type: DNA
A;Residues: 1-405 <STC>
A;Note: Similar to lipase; R11G11.14
C;Genetics:
A;Note: Similar to lipase; R11G11.14
A;Map position: 5
C;Superfamily: triacylglycerol lipase, lingual
                                                   A; Accession: T22290
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-411 <WIL>
A; Residues: 1-411 <WIL>
A; Residues: EMBL: 270780; PIDN: CAA94824.1; GSPDB: GN00023; CESP: F46B6.8
A; Experimental source: clone F46B6
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein F54F3.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
C;Accession: T226F5
F;Percy, C.; iloyd, C.
Submitted to the EMBL Data Library, September 1996
A;Reference number: 219598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 YWNWSWDDLVVNDLPAMVDFVVKQTGQKP-HYVGHSMGTLVA---LAAFSEGRVVSQLKS 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 YWNWSWDDLVVNDLPAMVDFVVKQTGQKP-HYVGHSMGTLVALAAFS--EGRVVSQLKSA 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 405;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 31.5%; Score 147.5; DB 2; Best Local Similarity 34.8%; Pred. No. 5.2e-09; Matches 32; Conservative 17; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31.1%; Score 145.5; DB 2
42.4%; Pred. No. 8.7e-09;
iive 13; Mismatches 22
                                                                                                                                                                                                                                                                                                                                            A)Gene: CESP:F46B6.8
A;Map position: 5
A;Introns: 35/3; 69/1; 104/1; 226/3
C;Superfamily: triacylglycerol lipase, lingual
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        198 YFALAPIGAVKNIKGFLSYFAHKFSPEFD-GW 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66 AALLIPV-----AYLXHXNXPNXNPGW 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                 A; Reference number: Z19542
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Best Local Similarity
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                                                                                                                                                                                                      A.Accession: S04942
A.Molecule type: protein
A.Residues: 20-45 < MERP
C.Superfamily: triacylglycerol lipase, extracellular protein; glycoprotein; lipid diges
E.Superfamily: triacylglycerol lipase; extracellular protein; glycoprotein; lipid diges
E.1-19/Domain: signal sequence #status predicted <SIG>
F.20-398/Product: triacylglycerol lipase, gastric #status experimental <MAMD>
E.34,99,185,271/Rainding site: carbohydrate (Asn) (covalent) #status predicted
A;Note: it is uncertain whether Met-1 or Met-7 is the intiator R:Bernbaeck, S.; Blaeckberg, L. Bur. J. Blochem. 182, 495-499, 1989
A;Title: Human gastric lipase. The N-terminal tetrapeptide is essential for lipid bindin A;Reference number: S04942; MUID:89325292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A.Cross-references: GB.X02309, NID:956595, PIDN:CAA26179.1; PID:956596
A.Experimental source: strain Sprague-Dawley
A.Note: the partial sequence of the mature protein from a different, unspecified strain
C.Comment: This acid-stable lipase is secreted by the serous (von Ebner's) glands at the
C.Superfamily: triacylglycerol lipase, lingual
C.Superfamily: triacylglycerol lipase, glycoprotein; lipid digestion; saliva; serous gl
F.1-18/Domain: signal sequence #status predicted <SIG-Nomain: signal sequence #status predicted <SIG-Nomain: signal sequence as the sequence described (SIG-Nomain) and sequence as the sequence for the second of the sec
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R; Docherty, A.J.P.; Bodmer, M.W.; Angal, S.; Verger, R.; Riviere, C.; Lowe, P.A.; Lyons, Nucleic Acids Res. 13, 1891-1903, 1985

A; Title: Molecular cloning and nucleotide sequence of rat lingual lipase cDNA.

A; Reference number: A23045; MUID:85215587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 11-Jun-1999
C;Accession: A23045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein F46B6.8 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 YWNWSWDDLVVNDLPAMYDFVVKQTGQ-KPHYVGHSMGTLVALAAFSEG-RVVSQLKSAA 67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Score 156; DB 2;
; Pred. No. 5.4e-10;
13; Mismatches 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               submitted to the EMBL Data Library, April 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31; Conservative
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196 ALAPVATVKYTQSP 209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 31; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-395 < DOC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  197 ALAPVA 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68 LLTPVA 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Accession: T22290
R; McMurray, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: A23045
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Gaps

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Typosomal acid lipase (EC 3.1.1.-) / sterol esterase (EC 3.1.1.13) precursor - human C; Species: Homo sapiens (man)
C; Date: 13-Jan-1995 **Requence_revision 13-Jan-1995 **text_change 18-Jun-1999
C; Accession: $41408; A39315; $47187
R; Ameis, D.; Merkel, M.; Eckerskorn, C.; Greten, H.
Eur. J. Biochem. 219, 905-914, 1994
A; Title: Purification, characterization and molecular cloning of human hepatic lysoso A; Accession: $41408; MUID:94155897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Anderson, R.A.; Sando, G.N.
J. Biol. Chem. 266, 22479-22484, 1991
A;Title: Cloning and expression of cDNA encoding human lysosomal acid lipase/choleste
A;Reference number: A39315; MUID:92042192
A;Stetus: preliminary
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A; Molecule type: mRNA
A; Residues: 1-15, Pr, 17-399 <AND>
A; Cross-references: GB M74775; NID:g187151; PIDN:AAA59519.1; PID:g187152
B; Du, H.; Gregory, G.A.
submitted to the EMBL Data Library, April 1994
A; Description: Structural conservation of putative functional motifs between mouse an A; Reference number: S47187
A; Accession: S47187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:AF067942; PIDN:AAC17694.1; GSPDB:GN00023; CESP:2K6.7 A;Experimental source: strain Bristol N2; clone 2K6
                                                       hypothetical protein 2K6.7 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A.Status: pressure Type: mRNA
A;Molecule type: mRNA
A;Residues: 1.399 <AME>
A;Cross-references: EMBL:X76488; NID:g434305; PIDN:CAA54026.1; PID:g434306
A;Cross-references: EMBL:X76488; NID:g434305; PIDN:CAA54026.1; PID:g434306
B;Anderson, R.A.; Sando, G.N.
T minl Chem. 266, 22479-22484, 1991
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A; Residues: 1-22, 'R', 24-399 <DUH>
A; Cross-references: EMBL: 231690; NID: 9506430; PIDN: CAA83495.1; PID: 9506431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 YWNWSWDDLVVNDLPAMVDFVVKQTGQ-KPHYVGHSMGTLVALAAFS--EGRVVSQLKSA 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4.2e-08;
ches 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
                                                                                                                                                                                                                                     A;Description: The sequence of C. elegans cosmid ZK6.
A;Reference number: 221301
A;Accession: T33198
                                                                                                                                                                                                                                                                                                                                 A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 139.5;
Pred. No. 4.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A Map position: 5
A;Introns: 29/3; 63/1; 219/3; 319/3; 365/3
C;Superfamily: triacylglycerol lipase, lingual
                                                                                                                                                                                                             May 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Gene: GDB:LIPA
A;Cross-references: GDB:120153; OMIM:278000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16;
                                                                                                                                                                                                          submitted to the EMBL Data Library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29.8%;
36.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       192 FALAPIGSVKH 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67 ALLTPVAYLXH 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-403 <WUX>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Status: preliminary
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                                                                                                                                                  C; Accession: T33198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
S41408
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C; Date: 1. U-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C; Accession: JC4017; S64678
R; Timmermans, M.Y.J; Teuchy, H.; Kupers, L.P.M.
A; Reference number: JC4017; MUID: 95011625
A; Accession: JC4017
A; Residues: 1.397 <TIM
A; Reference number: S64678; MUID: 96177869
A; Reference number: S64678; MUID: 96177869
A; Residues: 24-40; 248-253 <TIM>C; Comment: Pregastric esterase is a major fat-digesting enzyme.
C; Comment: Pregastric esterase is a major fat-digesting enzyme.
C; Comment: Pregastric esterase is a major fat-digesting enzyme.
C; Genetics: C; Superfamily: triacylglycerol lipase, lingual
C; Keywords: blocked amino end; carboxylic ester hydrolase; glycoprotein
C; Keywords: blocked amino end; carboxylic ester hydrolase; glycoprotein
C; Keywords: blocked amino end; carboxylic ester kistatus predicted
C; Superfamily: stianal sequence #status predicted (AMI)
F; 20-397/Product: pregastric esterase #status predicted (AMI)
F; 20-397/Product: pregastric esterase #status predicted (AMI)
F; 21/1/Active site: Ser #status predicted (ANI) (covalent) #status predicted
F; 171/Active site: Ser #status predicted
F; 171/Active site: Ser #status predicted
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                                                                                                                    PIDN:CAB01973.1; GSPDB:GN00023; CESP:F54F3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N;Alternate names: pregastric esterase
C;Species: Bos primigenius taurus (cattle)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 YWNWSWDDLVVNDLPAMVDFVVKQTGQKP-HYVGHSMGTLVALAAFSEGRV--VSQLKSA 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 YWNWSWDDLVVNDLPAMVDFVVKQTGQKP-HYVGHSMGTLVALAAFSEGRVVSQ-LKSAA 67
                                                                                                                                                                                                                                                                                                                                                                                     Length 405;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 397;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 triacylglycerol lipase (EC 3.1.1.3) PGE precursor - bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20;
                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31.0%; Score 145; DB 1; 42.4%; Pred. No. 9.7e-09;
                                                                                                                                                                                                                                                                                                                                                                                  31.1%; Score 145.5; DB 39.4%; Pred. No. 8.7e-09.
                           A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                            16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16; Mismatches
                                                                                                                                                                                                                               A;Map position: 5
A;Introns: 31/3; 65/1; 274/3; 366/3
C;Superfamily: triacylglycerol lipase, lingual
                                                                                                              A)Cross-references: EMBL:279696; P. A, Experimental source: clone F54F3 C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 42.49
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 39.48
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | || : |
FALAPVGSVKH 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67 ALLTPVAYLXH 77
                                                                                  A; Residues: 1-405 <WIL>
                                                                                                                                                                                                      A; Gene: CESP: F54F3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | |||
196 ALAPVA 201
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A; Accession: T22675
                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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A; Map position: 10q24-10q25

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F;228-229/Cleavage site: Arg-Asp (egg 30.5K cysteine proteinase) #status experimental
                                                                                                             26.9%;
                                                                                   Query Match
Best Local Similarity 33.89
                                                                                                                                                                                                                                                                                                                                                                                                                                                          |:|: |: : |
353 ALSPIVYMNYVRSP 366
                                                                                                                                                                                                                                                                                                                                                                                                                68 LLTPVAYLXHXNXP 81
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Best Local Similarity
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A. Molecule type: DNA
A. Residues: 1-59 csarx
A. Residues: 1-59 csarx
A. Residues: 1-59 csarx
A. Brol- Chem. 263. 1045-1051. 1988
A. Title: A unique protease responsible for selective degradation of a yolk protein in I A. Reference number: A2527: MUID:88087166
A. Residues: 19-40:133-144, T', 146-152; 229-248 <IND>
C. Cenetics:
A. Residues: 19-40:133-144, T', 146-152; 229-248 <IND>
A. Residues: 19-40:133-144, T', 146-152; 248 <
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C;Keywords: egg yolk; homotrimer
F:132-133/Cleavage site: Lys-Asn (egg 30.5K cysteine proteinase) #status experimental
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C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 18-Jun-1999
C;Accession: G01416
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C;Species: Bombyx mori (silkworm)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 26-Feb-1998
C;Accession: JT0949; A28527
R;Sato, Y: Yamashita, O.
submitted to JIPID, September 1991
A;Reference number: JT0949
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A; Accession: G01416
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-399 < DUX>
A; Cross-references: EMBL: U08464; NID: 9505052; PIDN: AAB60328.1; PID: 9505053
C; Superfamily: triacylqlycerol lipase, lingual
C; Keywords: 9lycoprotein
                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                               10 YWNWSWDDLVVNDLPAMVDFVVKQTGQKP-HYVGHSMGTLVALAAFSE-GRVVSQLKSAA 67
                                                                                                                                                                                                                       5;
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                                                                                                                                                   DB 2; Length 399;
                                                                                                                                               ; Score 136; DB 2; Length 39; Pred. No. 1e-07; 18; Mismatches 31; Indels
C;Superfamily: triacylglycerol lipase, lingual C;Keywords: carboxylic ester hydrolase; glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R,Du, H.
submitted to the EMBL Data Library, April 1994
                                                                                                                                           Query Match 29.1%;
Best Local Similarity 35.4%;
Matches 28; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       199 ALGPVASVAFCTSPMAKLG 217
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C; Species: Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Date: 10 - May-2001 #sequence_revision 10 - May-2001 #text_change 24 - May-2001
C; Accession: 689074
A; Title: Genome sequence of the nematode C. elegans: a platform for investigating bio A; Title: Genome sequence of the nematode C. elegans: a platform for investigating bio A; Meference number: A75000; MUID:99059613; PMID:9851916
A; Note: see websites genome wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_A; Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; A; Accession: G89074
A; Status: preliminary
A; Mescidues: 1-411 <STO>
A; Acsidues: 1-411 <STO>
A; Accession: G8: 1-411 <STO>
A; Cross-references: GB: chr_V; PIDN:AAC48051.1; PID:91658354; GSPDB:GN00023; CESP:K04A
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C;Accession: T20480
B;Hembry, C.
submitted to the EMBL Data Library, October 1996
A;Reference number: 219280
A;Reference number: 219280
A;Reference number: 219280
A;Resion: T20480
A;Resion: T20480
A;Resion: T20480
A;Resion: T20480
A;Resion: Fpe: DNA
A;Resion: 1-426 <WIL>
A;Resion: 
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                                                                                                                                                                                                                                                   10 YWNWSWDDLVVNDLPAMVDFVVKQTGQ-KPHYVGHSMGTLVALAAFSEGRVVSQ-LKSAA 67
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Length 559,
                                                                                                                                Indels
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; Score 126; DB 2;
; Pred. No. 2.1e-06;
19; Mismatches 28
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A;Introns: 29/3; 64/1; 186/3; 347/2
C;Superfamily: triacylglycerol lipase, lingual
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C;Superfamily: triacylglycerol lipase, lingual
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R; Hilbert, H: Duesterhoeft, A.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
aubmitted to the EMBL Data Library, August 1996
A; Reference number: 21967
A; Accession: T41053
A; Status: prellminary; translated from GB/EMBL/DDBJ
A; Status: prellminary; translated from GB/EMBL/DDBJ
A; Rosidues: 1-467 <HIL>A; Rossereferences: EMBL:AL031324; PIDN:CAA20447.1; GSPDB:GN00068; SPDB:SPCC1672.09
A; Experimental Source: strain 972h-; cosmid c1672
C; Genetics:
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142 FWDWSWDQISEYDLPAMIGKALEISGQESLYYTGFSLGTLTWFAKLSTDPKFSRKIKKYF 201
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Length 411;
Query Match 26.1%; Score 122; DB 2; Length 41 Best Local Similarity 33.3%; Pred. No. 4.3e-06; Matches 24; Conservative 17; Mismatches 29; Indels
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C;Superfamily: triacylglycerol lipase, lingual
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A:Introns: 12/2; 164/3; 294/1
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Search completed: October 10, 2002, 02:14:05 Job time: 213 sec

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; Sequence 42658, Application US/10219999; GENERAL INFORMATION:
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US-10-219-999-42658
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798.313 Million cell updates/sec
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110191,
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37594, A
36768, A
55922, A
126910,
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9393, Ap
89046, A
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                                                                                                              ; Search time 31.19 Seconds
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7: /cgn2_6/ptcdata/1/paa/USO8_NEW_COMB.pep:*
GenCore version 4.5
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US-10-219-999-52422
US-09-791-537-112004
US-09-791-537-122784
US-09-791-537-37594
US-09-791-537-37594
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US-10-219-999-54283
US-09-791-537-94868
US-10-056-744B-5
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                                                                                                                                                                                                                                                                                                                           1006125 seqs, 276659714 residues
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                                                                                                            October 10, 2002, 02:02:02
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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130374,
577, APP
65860, A
70755, A
87572, A
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62, Appl
63, Appl
64, Appl
65, Appl
130392,
73098, A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Cao, Yongwei APPLICANT: Cao, Yongwei APPLICANT: Cao, Yongwei APPLICANT: Cao, Yongwei APPLICANT: Edgerton, Michael D APPLICANT: Hinkle, Gregory J. APPLICANT: Kovalic, David K. APPLICANT: Liu, Jingdong APPLICANT: Stein, Joshua SEQUENCES AND USES FOR PLANT IMPROVEMENT: FILE OF INVENTION: CDN SEQUENCES AND USES FOR PLANT IMPROVEMENT: FILE REPRENCE: 38-10(52726)C; CURRENT FILING DATE: 2001-09-15

PRIOR APPLICATION NUMBER: US 60/312,544

PRIOR FILING DATE: 2001-09-21

PRIOR FILING DATE: 2001-08-15

NUMBER OF SEQ ID NOS: 63520

SEQ ID NO 43231
       Sednence Sed
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69.4%; Pred. No. 4e-27;
Live 12; Mismatches 10; Indels
US-09-759-130B-419

US-60-365-384-253

US-09-759-130B-417

US-09-791-537-130374

US-09-791-537-65860

US-09-791-537-65860

US-09-791-537-65860

US-09-791-537-65860

US-09-791-537-87572

US-00-791-537-87572

US-10-002-945-63

US-10-002-945-64

US-10-002-945-64

US-10-002-945-64

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US-10-002-945-67
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US-09-791-537-114140
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   68 LLTPVAYLXHXN 79.
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Matches 50; Conserv
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APPLICANT: Gao, Yongwei
APPLICANT: Edgerton, Michael D
APPLICANT: Hinkle, Gregory J.
APPLICANT: Kovalic, David K.
APPLICANT: Liu, Jingdong
APPLICANT: Stein, Joshua

APPLICANT: APPLICANT: APPLICANT: APPLICANT:

11:1:11 | 1 206 LLSPIAYLSHMN 217

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; ORGANISM: Zea mays
US-10-219-999-54283
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US-09-791-537-94868
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                    APPLICANT:
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GENERAL INFORMATION
APPLICANT: Cao, Yongwei
APPLICANT: Edgerton, Michael D
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Joshua
TITLE OF INVENTION: CDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT
FILE REPERENCE: 38-10/52726)C
CURRENT APPLICATION NUMBER: US/10/219,999
CURRENT APPLICATION NUMBER: US/10/219,999
CURRENT APPLICATION NUMBER: US/10/219,999
FRIOR FILING DATE: 2001-08-15
PRIOR FILING DATE: 2001-08-15
PRIOR FILING DATE: 2001-08-15
NUMBER OF SEQ ID NOS: 63520
SEQ ID NO 35161
LENGTH: 399
TITLE OF INVENTION: CDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT
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55.6%; Pred. No. 3.1e-21;
tive 12; Mismatches 20;
                                                                                                                                                                                                                                                                                                                 49.8%; Score 233; DB 6; 55.6%; Pred. No. 1.9e-21; ative 12; Mismatches 20
            FILE REFERENCE: 38 10 (52726) C
CURRENT APPLICATION NUMBER: US/10/219, 999
CURRENT FILING DATE: 2002-08-15
PRIOR APPLICATION NUMBER: US 60/324,109
PRIOR FILING DATE: 2001-09-21
PRIOR FILING DATE: 2001-09-21
PRIOR FILING DATE: 2001-09-21
NUMBER OF SEQ ID NOS: 63520
SEQ ID NO 43658
LENGTH: 266
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US-10-219-999-54283
US-10-219-999-54283
Sequence 54283, Application US/10219999
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
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Best Local Similarity 55.6%
Matches 40; Conservative
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Best Local Similarity 55.6
Matches 40; Conservative
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196 CPIAHLNHVTSP 207
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63 CPIAHLNHVTSP 74
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Sequence 94868 Application US/09791537
GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
TITLE OF INVENTION: METHODS OF USE THEREOF
CURRENT APPLICATION UMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SEQ ID NO 94868
LENGTH: 394
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                                                                  APPLICANT: Liu, Jingdong
APPLICANT: Stein, Joshua
TITLE OF INVENTION: CDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT
FILE REFERENCE: 38-10(52726)
CURRENT APPLICATION NUMBER: US/10/219,999
CURRENT FILING DATE: 2002-08-15
PRIOR PELLING DATE: 2001-09-21
PRIOR FILING DATE: 2001-09-21
PRIOR FILING DATE: 2001-08-15
PRIOR FILING DATE: 2001-08-15
NUMBER FUL SEQ ID NOS: 63520
SEQ ID NO 54283
LENGTH: 393
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44.2%; Pred. No. 1.4e-14;
tive 15; Mismatches 28; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Drosophila melanogaster
US-09-791-537-94868
Edgerton, Michael
Hinkle, Gregory J.
Kovalic, David K.
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Best Local Similarity 44.2%
Matches 34; Conservative
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181 KMISSAALLCPISYLDH 197
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Sequence 122314, Application US/09791537
GENERAL INFORMATION:
APPLICANT: Blonomix. Inc.
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: METHODS OF USE THEREOF
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REPRENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILE SAID NOS: 153055
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 122314
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APPLICANT: Blonomix, Inc.
APPLICANT: Blonomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REPERENCE: 251/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT APPLICATION NUMBER: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PatentIn version 3.0
SEC ID NO 93233
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110 FWAFSFDEMAKYDLPATIDFIVKKTGQKQLHYVGHSQGTTIGFIAFSTNPSLAKRIKTFY 169
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Pred. No. 2.3e-11;
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       CURRENT APPLICATION NUMBER: US/09/791,537
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                        CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PatentIn version 3.0
SEQ ID NO 50507
LENGTH: 371
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Best Local Similarity 47.0%;
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US-09-791-537-50507
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| 191 ALAPVA 196
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APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SSOFTWARE: Patentin version 3.0
SSOFTWARE: Patentin version 3.0
LENGTH: 344
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APPLICANT: Danzer, Joseph
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: HTREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
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                                                                                                                                                                                                                                                                                                                                                                                       Length 127;
TITLE OF INVENTION: 58860, A HUMAN CHOLESTERYL ESTER TITLE OF INVENTION: HYDROLASE AND USES THEREFOR FILE REFERENCE: MPI2001-026PIRNM
                                                                                                                                                                                                                                                                                                                                                                                  Query Match 36.3%; Score 170; DB 6; Best Local Similarity 45.9%; Pred. No. 9.3e-14; Matches 34; Conservative 14; Mismatches 24
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                                                                  CURRENT APPLICATION NUMBER: US/10/056,744B
CURRENT FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: 60/264,167
PRIOR FILING DATE: 2001-01-25
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-791-537-49394
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105 ALAPVAYMKHVRSP 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68 LLTPVAYLXHXNXP 81
                                                                                                                                                                                                                                                                                     CRGANISM: Homo sapiens US-10-056-744B-5
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192 CPISYLDHVTAP 203
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Best Local Similarity
Matches 28; Conserva
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US-09-791-537-50507
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10 YWNWSWDDLVVNDLPAMVDFVVKQTGQKP-HYVGHSMGTLVALAAFSEG-RVVSQLKSAA 67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-002-945-66
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                                                                                                                                                                    68 LLTPVA 73
                                                                                                                                                                                                                                                                                                                                                                   US-10-002-945-66
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APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Prasar, Christopher C
APPLICANT: Barnes, Thomas S
APPLICANT: Millen, Sann J
APPLICANT: Millen, 
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137 FWAFSFDEMAKYDLPATIDFIVKKTGQKQLHYVGHSQGTTIGFIAFSTNPSLAKRIKTFY 196
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47.0%; Pred. No. 2.4e-11;
tive 13; Mismatches 20; Indels
                                                                                                                                                                                                  DB 5; Length 398;
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                                                                                                                                                                                               33.3%; Score 156; DB 5; 47.0%; Pred. No. 2.4e-11;
                                                                                                                                                                                                                                     ; Pred. No. 2.4e
13; Mismatches
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GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 445 LENGTH: 398
                                                                                                                                                                                                                                                                   31; Conservative
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Sest Local Similarity 47.0
Matches 31; Conservative
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                              ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-93233
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Best Local Similarity
Matches 31; Conserv
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197 ALAPVA 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                68 LLTPVA 73
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US-09-759-130B-445
LENGTH: 398
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APPLICANT: Verlie, Collie A M
APPLICANT: Casman, Stacie J
APPLICANT: Casman, Stacie J
APPLICANT: Stacie J
APPLICANT: Shory, Suresh G
APPLICANT: Baumgartner, Jason C
APPLICANT: Baumgartner, Jason C
APPLICANT: Colman, Steven D
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-206
CURRENT APPLICATION NUMBER: US/10/002,945
CURRENT FILING DATE: 2000-11-02
PRIOR PELING DATE: 2000-11-02
PRIOR APPLICATION NUMBER: 60/245,317
PRIOR APPLICATION NUMBER: 60/246,562
PRIOR APPLICATION NUMBER: 60/246,562
PRIOR PILING DATE: 2000-11-07
PRIOR PILING DATE: 2000-11-08
PRIOR FILING DATE: 2001-01-08
PRIOR FILING DATE: 2001-01-08
PRIOR PELING DATE: 2001-01-08
PRIOR PELING DATE: 2001-01-26
PRIOR PELING DATE: 2001-01-26
PRIOR PELING DATE: 2001-01-26
PRIOR FILING DATE: 2001-01-26
SOFTWARE: PALENTIN VET: 2.1
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Sequence 66, Application US/10002945 GENERAL INFORMATION:
                                                                          MacDougall, John R
Smithson, Glannda
Millet, Isabelle
Stone, David
Gunther, Erik
Ellerman, Karen
Alsobrook II, John P
                                                                                                                                                                                                                                                                                                                                                                                     Gorman, Linda
Taupier Jr, Raymond J
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Guo, Xiaojia (Sasha)
Fernandes, Elma R
Vernet, Corine A M
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Burgess, Catherine
Spytek, Kimberly A
                                                                                                                                                                                                                                                                                                                                   Edinger, Shlomit
Gangolli, Esha A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 33.3%
Best Local Similarity 47.09
Matches 31; Conservative
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Gaps

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Sequence 122784, Application US/09791537

SEQUENCE 122784, Application US/09791537

GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
TITLE OF INVENTION: HEREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
STATEMENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SEQ ID NO 122784
LENGTH: 395
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136 FWAFSFDEMAKYDLPATINFIVOKTGQEKIHYVGHSQGTTIGFIAFSTNPTLAKKIKTFY 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32.5%; Score 152; DB 5; 40.5%; Pred. No. 7.6e-11;
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Job time: 577 sec
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196 ALAPVATVKYTQSP 209
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Best Local Similarity
  197 ALAPVA 202
                                                                         RESULT 15
US-09-791-537-122784
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APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
LENGTH: 398
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137 FWAFSFDEMAKYDLPATIDFIVKKTGQKQLHYVGHSQGTTIGFIAFSTNPSLAKRIKTFY 196
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APPLICANT: Edgerton, Michael D
APPLICANT: Binkle, Gregory J.
APPLICANT: Kovalic, David K.
APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Liu, Joshua
TITLE OF INVENTION: CDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT
FILE REFERENCE: 38-10(22726)C
CURRENT APPLICATION NUMBER: US/10/219,999
CURRENT FILING DATE: 2002-08-15
PRIOR FILING DATE: 2001-09-21
PRIOR FILING DATE: 2001-08-15
PRIOR FILING DATE: 2001-08-15
NUMBER: OF SEQ ID NOS: 63520
LENGTH: 182
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Pred. No. 1.2e-11;
0; Mismatches 5;
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GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
                                                                                                                                                                                         US-10-219-999-52422
; Sequence 52422, Application US/10219999
; GENERAL INFORMATION:
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86.8%;
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Best Local Similarity 86.88
Matches 33; Conservative
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                                                                                                                                                                                                                                                                          APPLICANT: Cao, Yongwei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Zea mays
US-10-219-999-52422
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197 ALAPVA 202
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                                                 68 LLTPVA 73
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165.162 Million cell updates/sec
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Appli
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1 SSCTLRFQLYWNWSWDDLVV......pvaylxhxnxpnxnpgwpxr
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24HHHH32223888444	ALI 18, Application US/08227108 5, 5807726 INFORMATION: ANT: Blanchard, Claire ANT: Benicourt, Claude ANT: Benicourt, Claude ANT: Benicourt, Claude ANT: Benicourt, Claude ANT: Unien, Jean-Louis OF INVENTION: Recombinant D R OF SEQUENCES: 21 SPONDENCE ADDRESS: EET: 1155 Avenue of the Amer F: New York FE: New York TE: New York	tch al Similarity 47.0%; Score 158; DB 1; Length 379; al Similarity 47.0%; Pred. No. 1.2e-13; 31; Conservative 14; Mismatches 19; Indels 2; G XWNWSWDDLVVNDLPAMVDFVVKQTGQ-KPHYVGHSMGTLVALAAFSEG-RVVSQLKSAA	= :: :: :: :: :: :: :: :: :: :: :: :: ::
σσοοοοοοοοοοοοοοοοοοοοοοοοοοοοοοοοοοο	T 1 -277-108-18 uence 18, Application US/087 ent No. 5807726 NERAL INFORMATION: APPLICANT: Benicourt, Clau APPLICANT: Benicourt, Clau APPLICANT: Benicourt, Clau APPLICANT: Dunien, Jean-Lot TITLE OF INVENTION: NUMBER OF SEQUENCES: 21 CORRESPONDENCE ADDRESS: ADDRESSEE: Pennie & Edmor STREET: 1155 Avenue of th CITY: New York COUNTRY: U.S.A. ZIP: 10036 COMPUTER: IBM FC COMPALIN MEDIUM TYPE: Floppy disk COMPUTER: IBM FC COMPALIN OPERATING SYSTEM: OS-AR-1994 COMPUTER: DAPLICATION DATA: APPLICATION NUMBER: US/06 FLILING DATE: 03-APR-1994 ATTORNEY/AGENT INFORMATION: NAME: FANDENCI, Allan A. REGISTRATION NUMBER: 30, AREFERENCE/POCKET NUMBER: TELEFHON: 212 869-8864/970 TELEFHON: SEQ ID NO: 16 STRANDEDMESS: SINGLE TOPOLOGY: linear MOLECULE TYPE: protein	33.8% 47.0% ive MVDFV	=
1479 1479 1480 1480 1480 1480 1480 1480 1480 1480	pplication US/7726 MATION: Blanchard, Cl Benicourt, Cl Benicourt, Cl Benicourt, Cl Benicourt, Cl Benicourt, Cl Benicourt, Cl WI YORK U.S.A. 1155 Avenue of WY YORK U.S.A. 1155 Avenue of WY YORK U.S.A. 1155 Avenue of SYSTEM: PE: Floppy di SYSTEM: PE: Floppy di SYSTEM: PE: Floppy di SYSTEM: PE: Floppy di SYSTEM: ON NOWBER: U.ICATION DATA: ON NUMBER: U.ICATION DATA: ON NUMBER: U.ICATION DATA: ON NUMBER: U.ICATION OCH U.S.A. 379 amino acid U.S.A. 379 amino acid U.S.A. SINGLE U.S. SINGLE U.S	33. Larity 47. Conservative DLVVNDLPAMVD	Ξ
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22222222222222222	SULT 1 -08-277-108-18 Sequence 18, Application US Patent No. 5807726 GENERAL INFORMATION: APPLICANT: Blanchard, C APPLICANT: Benicourt, C APPLICANT: Benicourt, C APPLICANT: Junien, Jean TITLE OF INVENTION: Rec NUMBER OF SEQUENCES: 21 CORRESPONDENCE ADDRESS: ADDRESSEE: Pannie & E STREET: 1155 Avenue o CITY: New York STATE: New York STATE: New York COMPUTER: LIBM PC COMP COMPUTER: LIBM PC COMP COMPUTER: PatentIN Re COMPUTER: PatentIN REP COMPUTER: PatentIN ARP APPLICATION NUMBER: U TELEPHONE: 212 769-9864 TELECHONEN: ASO ID NO: SEQUENCE CHARACTERISTICS LENGTH: 379 amino aci TYPE: ADDRESS: Single TOPOLOGY: linear MOLECULE TYPE: Protein	Similarity 1; Conser WSWDDLVVND	:: :: ::
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נו נ	SULT 1 -08-227-108-18 Sequence 18, App. Patent No. 58077; GENERAL INFORMAR APPLICANT: B APPLICANT: D COMPUTER: New STATE: New COMPUTER: New STATE: New APPLICATION FILING DATE CLASSIFICATION REGISTRATION REGISTRATION TELEPHONE TELEPH	Ouery Match Best Local Matches 3	
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ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
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ATTORNEY/AGENT INFORMATION:
NAME: Fanucci, Allan A.
REGISTRATION NUMBER: 30,256
STATEMENT NUMBER: 7620-033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/073,674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/09073674 Patent No. 5998189
                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2800 Plymouth Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 379 amino acids
TYPE: amino acid
 NUMBER OF SEQUENCES: 21
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MOLECULE TYPE: protein
US-08-227-108-3
                     CORRESPONDENCE ADDRESS:
                                                                         New York
: New York
RY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 2800 Ply CITY: Ann Arbor STATE: Michigan
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                                                                         CITY: Nev STATE: Ne COUNTRY:
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US-09-073-674-3
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ZIP: 48105.

ZIP: 48105.

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/073,674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/08227108
Patent No. 5807726
GENERAL INFORMATION:
APPLICANT: Balanchard, Claire
APPLICANT: Benicourt, Claude
APPLICANT: Junien, Jean-Louis
(TITLE OF INVENTION: Recombinant Dog Gastric Lipase
                                                                                                                                                                                                                         APPLICANT: Blanchard, Claire
APPLICANT: Benicourt, Claude
APPLICANT: Junien, Jean-Louis
TITLE OF INVENTION: Recombinant Dog Gastric Lipase
CORRESPONDENCES: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 158; DB 2;
Pred. No. 1.2e-13;
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                                                                                                                                                                                                                                                                                                                                                Warner-Lambert Company
                                                                                                                                                                  Sequence 18, Application US/09073674 Patent No. 5998189 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: CISSEN, TOOM M.
REGISTRATION NUMBER: 37,807
REFERENCE/DOCKET NUMBER: 5072
TELECOMMUNICATION INFORMATION:
TELEPHONE: 734 622-7530
TELEPHONE: 734 622-1553
                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Warner-Lambert (STREET: 2800 Plymouth Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 18:
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Best Local Similarity 47.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 379 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                 CITY: Ann Arbor
STATE: Michigan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Blanchard, Claire
APPLICANT: Benicourt, Claude
APPLICANT: Junien, Jean-Louis
TITLE OF INVENTION: Recombinant Dog Gastric Lipase
NUMBER OF SEOFENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Warner-Lambert Company
COMPUTER READABLE FORM:

COMPUTER: Floppy disk

COMPUTER: IBM PC Compatible

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTIN Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/227,108

FILING DATE: 03-APR-1994

CLASSIFICATION: 435
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Gaps
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32.9%; Score 154; DB 1; Length 380; 45.5%; Pred. No. 4.4e-13; tive 15; Mismatches 19; Indels
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45.5%; Pred. No. 4.4e-13;
tive 15; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                             Sequence 5, Application US/09073674
Patent No. 5998189
GENERAL INFORMATION:
APPLICANT: Blanchard, Claire
APPLICANT: Benicourt, Claude
APPLICANT: Uniten, Jean-Louis
TITLE OF INVENTION: Recombinant Dog Gastric Lipase
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Warner-Lambert Company
STREET: 2800 Plymouth Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: Michigan
COMPRY: U.S.A.
2IP: 48105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/073,674
FILING DATE:
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10S-08-227-108-17
Sequence 17, Application US/08227108
Patent No. 5807726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Clissey, Todd M.
REGISTRATION NUMBER: 37,807
REFERENCE/POCKET NUMBER: 5072
TELECOMMUNICATION INFORMATION:
TELEPHONE: 734 622-7530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 380 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; MOLECULE TYPE: protein US-09-073-674-5
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Best Local Similarity
Ouery Match
Best Local Similarity
Matches 30; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ann Arbor
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                                                                                                                                                                       68 LLTPVA 73
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US-09-073-674-5
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118 FWAFSFDEMAKYDLPATIDFILKKTGQDKLHYVGHSQGTTIGFIAFSTNPKLAKRIKTFY 177
                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                             Length 379;
                                                                                                                                                                                                                                                                                                                                                             32.9%; Score 154; DB 2; Length 37:
45.5%; Pred. No. 4.4e-13;
Live 15; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5, Application US/08227108
Patent No. 5807726
GENERAL INFORMATION
APPLICANT: Blanchard, Claire
APPLICANT: Benicourt, Claude
APPLICANT: Junien, Jean-Louis
TITLE OF INFORTION: Recombinant Dog Gastric Lipase
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: PIB PC compatible
COMPUTER: PER PRESENT FC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/227,108
FILING DATE: 03-APR-1994
CLASSIFICATION: 435
                                                               5072-D1-66-TMC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY AGENT INFORMATION:
NAME: Fanucci, Allan A.
REGISTRATION NUMBER: 30,256
REFERENCE/DOCKET NUMBER: 7620
TELECOMMUNICATION INFORMATION:
TELEFAX: 212 869-8084/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 300 amino acids
TYPE: amino acid
                   NAME: Crissey, Todd M.
REGISTRATION NUMBER: 37,807
REFERENCE/DOCKET NUMBER: 5072
TELECOMMUNICATION INFORMATION:
TELEPHONE: 734 622-7530
TELEFAX: 734 622-1553
                                                                                                                                                                INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 379 amino acids
TYPE: amino acid
TOPOLOGY: linear
  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                             Query Match 32.99
Best Local Similarity 45.59
Matches 30; Conservative
                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: protein US-09-073-674-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-227-108-5
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| 178 ALAPVA 183
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10 YWNWSWDDLVVVNDLPAMYDFVVKQTGQ-KPHYVGHSMGTLVALAAFSEG-RVVSQLKSAA 67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Blanchard, Claire
APPLICANT: Benicourt, Claude
APPLICANT: Junien, Jean-Louis
TITLE OF INVENTION: Recombinant Dog Gastric Lipase
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PLILOATION NUMBER: US/08/227,108
FILING DATE: 03-APR-1994
                               PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32.5%; Score 152; DB 2; 40.5%; Pred. No. 8.2e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 32.5%; Score 152; DB Best Local Similarity 40.5%; Pred. No. 8.2e Matches 30; Conservative 17; Mismatches
                                                                                                                                                                                                                                                                               5072-D1-66-TMC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/073,674
                                                                                 APPLICALL...
FILING DATE:
CLASSIFICATION:
ATTORNEY AGENT INFORMATION:
NAME: CTISSEY, TOdd M.
REGISTRATION NUMBER: 37,807
REFERENCE/DOCKET NUMBER: 5072
TELECOMMUNICATION INFORMATION:
THE PERCHANGE TO THE TOWNER TO
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ATTORNEY, AGENT INFORMATION:
NAME: FADUCCI, ALIAN A..
REGISTRATION NUMBER: 30,256
REFERENCE/DOCKET NUMBER: 7620
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 869-8864/9741
TELEFAX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 377 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: linear; MOLECULE TYPE: protein US-09-073-674-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       178 ALAPVATVKYTQSP 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Blanchard, Claire
APPLICANT: Benicourt, Claude
APPLICANT: Junien, Jean-Louis
IUTLE OF INVENTION: Recombinant Dog Gastric Lipase
CORRESPONDENCES: 21
                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION DATA:
APPLICATION DATA:
FILING DATE: 03-APR-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY AGENT INCORMATION:
NAME: Fanucci, Allan A.
REGISTRATION NUMBER: 30,256
REFERENCE/DOCKET NUMBER: 7620-033
TELECOMMUNICATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                         1155 Avenue of the Americas
                                                                                                                                                                                                         Pennie & Edmonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 377 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-227-108-17
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178 ALAPVATVKYTQSP 191
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CITY: Ann Arbor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Michigan
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GENERAL INFORMATION:
                                                                                                                                                                                                                               STREET: 1155 A. CITY: New York
                                                                                                                                                                                                                                                                                                                                 COUNTRY: U
                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: M. COUNTRY:
                                                                                                                                                                                                                                                                                                     STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         qq
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5 LRFQLYWNWSWDDLVVNDLPAMVDFVVKQTGQKP-------HYVGHSMGTLVAL 51
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                                                                                                   US-08-90-954-4

Sequence 4, Application US/08909954A

Sequence 4, Application US/08909954A

Patent No. 6100058

GENERAL INFORMATION:

APPLICANT: Allen, Maxine J.

TITLE OF INVENTION: GAP12 Genes and their Uses

FILE REFERENCE: SEQ-11P

CURRENT APPLICATION NUMBER: US/08/909,954A

CURRENT FILING DATE: 1997-08-12

NUMBER OF SEQ ID NOS: 15

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4225 EXECUTIVE SQUARE, STE 1400
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APPLICATION NUMBER: US/08/602,359A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 35, Application US/08602359A Patent No. 5942430 GENERAL INFORMATION:
APPLICANT: ROBERTSON, Daniel E. APPLICANT: MURPHY, Dennis
APPLICANT: REID, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INCH DISKETTE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: REID, John
APPLICANT: MAFFIA, Anthony
APPLICANT: LINK, Stewen
APPLICANT: SWANSON, Ronald V.
APPLICANT: WARREN, PATLICK V.
APPLICANT: WORNOTKA, Anna
TITLE OF INVENTION: ESTERASES
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 6.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: February
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: LA JOLLA
STATE: CALIFORNIA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: M. musculus
US-08-909-954-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 11:
253 VRLTEDRVL 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52 AAFSEGRVV 60
                                           178 YALAPVA 184
            67 ALLTPVA 73
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US-08-602-359A-35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 799
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                                                                                                                                                                  DB 1; Length 380;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 16, Application US/09073674
Patent No. 5998189
GENERAL INFORMATION
FAPPLICANT: Blanchard, Claire
APPLICANT: Benicourt, Claude
APPLICANT: Junian, Jean-Louis
TITLE OF INVENTION: Recombinant Dog Gastric Lipase
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marner-Lambert Company
STREET: 2800 Plymouth Road
                                                                                                                                                            31.1%; Score 145.5; DB 1;
46.3%; Pred. No. 6.6e-12;
tive 13; Mismatches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/073,674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5072-D1-66-TMC
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NAME: Crissey, Todd M.
REGISTRATION NUMBER: 37,807
REFERENCE/DOCKET NUMBER: 5077
TELECOMMUNICATION INFORMATION:
TELEPHONE: 734,622-7530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 16:
LENGTH: 380 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 380 amino acids
TYPE: amino acid
                                                                                                                                                              Query Match
Best Local Similarity 46.3%
Matches 31; Conservative
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Ann Arbor
STATE: Michigan
COUNTRY: U.S.A.
ZIP: 48105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 31; Conserva
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CLASSIFICATION:
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| 178 YALAPVA 184
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                                                                                                                                                                                                                                                                                                                         67 ALLTPVA 73
                                                                                                     US-08-227-108-16
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ZIP: COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                     TELEX: none
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS: Joernvall, H.
                                                                                                                                                                                                                                                                                                                                                                                                       protein
                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PAGES: 4226-4230
DATE: 1981
                                                                                                                                                                                                                                                                                                                                                                                                                      ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
DESCRIPTION:
                      none
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STATE: M.
COUNTRY:
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US-08-095-734-2
                                                                                                                                                                                                                                                                                                                                     LENGTH:
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Patent No. 5958784
GENERAL INFORMATION:
GENERAL INFORMATION:
FAPLICANT: Benner. Steven A.
TITLE OF INVENTION: Predicting Folded Structures of Proteins NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: Steven A. Benner
STREET: Hadlaubstrasse 151
                                                                                                                                                                                                                                                    DB 2; Length 262;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 3; Length 804;
                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                     13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/08909954A
Patent No. 6100058
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION GAPI2 Genes and their Uses
FILE REFERENCE: SEQ-11P
CURRENT APPLICATION NUMBER: US/08/909,954A
CURRENT FILING DATE: 1997-08-12
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                   14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13.8%; Score 64.5; D
ilarity 30.0%; Pred. No. 2.8;
Conservative 6; Mismatches
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                                                                                                                                                                                                                                                  Score 65.5;
Pred. No. 0.
                                09010/010001
                 REGISTRATION NUMBER: 38,347
REPERRICE/DOCKET NUMBER: 09
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-678-5070
                                                                             TELEFAX: 619-678-5090
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 262 AMINO ACIDS
TYPE: AMINO ACID
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1 Similarity 32.4%;
24; Conservative 1.
                                                                                                                                                               TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
HAILE, LISA A.
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131 IGYPLAKILASIAY 144
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ORGANISM: H. sapiens
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253 KVRLIEDRVL 262
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Best Local Similarity
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Best Local Similarity
Matches 21; Conserv
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                                                                                                                                                                                                   US-08-602-359A-35
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LENGTH: 804
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US-08-909-954-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-909-954-2
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STATE: not constructed by the control of the contro
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COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: TEM PC-DOS/MS-DOS
COFFWARE: Peacent RC-DOS/MS-DOS
COFFWARE: Peacent RC-DOS/MS-DOS
COFFWARE: Peacent RC-DOS/MS-DOS
CLASSIFICATION DATA:
CLASSIFICATION NUMBER: US/08/095,734
FILING DATE: 22-JUL-1993
CLASSIFICATION: NUMBER: US/08/095,734
FILING DATE: 23-JUL-1993
CASSIFICATION: NUMBER: WH193-11M
REGISTRATION NUMBER: WH193-11M
FELECHONE: Granahan. Perticia
REGISTRATION NUMBER: WH193-11M
FELECHONE: G17-861-940
FILING DATE: TIPE: DATE: US/08-0940
FILING DATE: US/08-0940
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